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OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 22:42:09 : Search time 79 Seconds  
(Without alignments)  
8200.505 Million cell updates/sec

Title: US-09-964-678A-1  
Perfect score: 1442  
Sequence: 1 ttttttttttgatgag.....ttaacaagcttagagca 1442

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 396772 seqs, 224632407 residues

Total number of hits satisfying chosen parameters: 793544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Published Applications, NR.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1442	100.0	1442	9 US-10-146-130-1	Sequence 1, Appl1
2	1442	100.0	1442	10 US-09-964-666-1	Sequence 1, Appl1
3	1442	100.0	1442	10 US-09-964-412-1	Sequence 1, Appl1
4	1223.4	84.8	1418	10 US-09-964-666-1	Sequence 4, Appl1
5	1223.4	84.8	1418	10 US-09-964-412-4	Sequence 4, Appl1
6	1080.2	74.9	1381	10 US-09-964-666-3	Sequence 3, Appl1
7	1080.2	74.9	1381	10 US-09-964-412-3	Sequence 3, Appl1
8	587.8	40.8	65608	9 US-09-954-531-180	Sequence 180, App
9	587.8	40.8	65608	10 US-09-962-436-292	Sequence 292, App
10	587.8	40.8	65608	10 US-09-962-832-119	Sequence 119, App
11	524.4	36.4	62944	10 US-09-954-456-1257	Sequence 2257, App
12	513	33.6	21470	10 US-09-964-847-1157	Sequence 1157, App
13	490.4	34.0	99014	10 US-09-880-107-3428	Sequence 3428, App
14	479.2	33.2	51719	10 US-09-918-686-2	Sequence 2, Appl1
15	479.2	33.2	92139	10 US-09-918-686-1	Sequence 1, Appl1
16	475.4	33.0	14796	10 US-09-954-456-973	Sequence 973, App
17	475.4	33.0	14796	10 US-09-954-456-1636	Sequence 1636, App
18	475.4	33.0	14796	10 US-09-918-186A-3	Sequence 3, Appl1
19	475.4	33.0	14796	10 US-09-880-107-3421	Sequence 3421, App

20	475.4	33.0	26657	10 US-09-810-673A-3	Sequence 3, Appl1
21	471.2	32.7	12542	10 US-09-764-864-1774	Sequence 1774, App
22	467	32.4	15041	10 US-09-764-869-1421	Sequence 1421, App
23	464.8	32.2	57130	10 US-09-835-081-3	Sequence 3, Appl1
24	447.8	31.1	14176	10 US-09-764-864-1644	Sequence 1644, App
25	440.8	30.6	13224	10 US-09-764-853-897	Sequence 897, App
26	440.2	30.5	110096	10 US-09-880-107-1542	Sequence 1542, App
27	439.2	30.0	110096	10 US-09-880-107-1542	Sequence 1542, App
28	433.2	30.0	20247	10 US-09-764-877-2680	Sequence 2680, App
29	429.8	29.8	27148	10 US-09-764-860-1046	Sequence 1046, App
30	426	29.5	32204	10 US-09-764-855-328	Sequence 328, App
31	426	29.5	32204	10 US-09-764-855-327	Sequence 327, App
32	425.6	29.5	24533	9 US-09-764-853-377	Sequence 1349, App
33	425.6	29.5	34641	10 US-09-954-456-1110	Sequence 1110, App
34	425.6	29.5	34641	10 US-09-954-456-1187	Sequence 1187, App
35	421	29.2	65464	9 US-09-859-888-3	Sequence 3, Appl1
36	420.6	29.2	2109	10 US-09-764-855-325	Sequence 38, Appl
37	420.6	29.2	17200	10 US-09-764-877-3390	Sequence 39, Appl
38	419.8	29.1	48436	10 US-09-927-602-38	Sequence 8, Appl1
39	419.2	29.1	6439	9 US-09-790-852-8	Sequence 1, Appl1
40	419.2	29.1	75270	9 US-09-790-852-1	Sequence 1733, App
41	418.4	29.0	21606	10 US-09-764-869-1733	Sequence 1, Appl1
42	417.2	28.9	133893	9 US-10-161-510-1	Sequence 1, Appl1
43	414.4	28.7	38374	10 US-09-880-107-3463	Sequence 3463, App
44	413.2	28.7	7233	10 US-09-764-865-2123	Sequence 2123, App
45	412.8	28.6	17792	10 US-09-764-869-1599	Sequence 1599, App

## ALIGNMENTS

RESULT 1  
US-10-146-130-1  
Sequence 1, Appl1  
Publication No. US20030004107A1  
GENERAL INFORMATION:  
APPLICANT: AVERACK, PAUL  
TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF  
FILE REFERENCE: 59003.000007  
CURRENT APPLICATION NUMBER: US/10/146.130  
CURRENT FILING DATE: 2002-08-06  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 1442  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (15)..(1139)  
US-10-146-130-1

Query Match	Best Local Similarity	Score	DB 9:	Length	1442:
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QY	61	TCTAGGTCACCGCAACCTCCGCTCCGCGTTCAACGATTCCTGCTCAGCTCCG	120		
DB	61	TCTAGGTCACCGCAACCTCCGCTCCGCGTTCAACGATTCCTGCTCAGCTCCG	120		
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DB	121	CAGTAGCTGCGATTACAGCGATGTCACCGACGCTGCGTAATTTGTATTTTAA	180		
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QY 1441 CA 1442
Db 1441 CA 1442

RESULT 2
US-09-964-666-1
; Sequence 1, Application US/09964666
; Patent No. US20020104108A1
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; Wands, Jack R.
; TITLE OF INVENTION: Transgenic Animals and Cell Lines for
; Screening Drugs Effective for the Treatment or Prevention
; of Alzheimer's Disease
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESS: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/964,666
; FILING DATE: 28-Sep-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmund, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0609.4370000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2500
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1442 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..1139
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-964-666-1

Query Match 100.0%; Score 1442; DB 10; Length 1442;
Best Local Similarity 100.0%; Pred. No. 7.2e-293;
Matches 1442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1441 CA 1442  
Db 1441 CA 1442

## RESULT 4

US-09-964-666-4

Sequence 4, Application US/09964666

Patent No. US20020104108A1

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

Wands, Jack R.

TITLE OF INVENTION: Transgenic Animals and Cell Lines for

Screening Drugs Effective for the Treatment or Prevention

of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS: Sterne, Kessler, Goldstein &amp; Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/964,666

FILING DATE: 28-Sep-2001

CLASSIFICATION: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0609.4370000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2540

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1418 base pairs

TYPE: nucleic acid

MOLECULE TYPE: cDNA

STRANDEDNESS: both

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Query Match 84.8%; Score 1223.4; DB 10; Length 1418;  
Best Local Similarity 96.9%; Pred. No. 3.5e-247;  
Matches 1375; Conservative 0; Mismatches 31; Indels 13; Gaps 12;



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Db 61 CTCAGCTACACGCAACCTCCGCTCCGCGGTTCAAGGATTTCTTCCCTCAGCTCCCC 120
QY 122 AGTA-GCTGGAGATTACAGGCAATGTGACCCCGCTGCTAATTTTATTTTATTTAG 180
Db 121 AGTAGGCTGGAGATTACAGGCAATGTGAC-CCAGCTCCGCTAATTTTATTTTATTTAG 179
QY 181 TAGAGATGAGATTCTCCATGTGTGCTAGGCTGTCTCGAATCCCGACTCAATATATC 240
Db 180 TAGAGATGAGATTCTCCATGTGTGCTAGGCTGTCTCGAAT-CCGACTCAATATATC 238
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Db 898 GCTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 957
QY 956 GCAATGCGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1015
Db 958 GCAATGCGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1017
QY 1016 TCTCAGCTCCCAAGCAGCTGAGATTACGGGACACTGCGACACACCCGCTAATTTTGTG 1075
Db 1018 TCTCAGCTCCCAAGCAGCTGAGATTACGGGACACTG-CACACACACCCGCTAATTTTGTG 1076
QY 1076 TATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1135

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Db 1077 TATTTTATTTATGAGGCGGCTTTCAACATATTTGTGAGGCTGTCTCAAACTCTGACT 1136
QY 1136 CAGGTGACCCACCTGCTCAGCTTCCAAAGTGTGGGATTACAGGCTGGACACCTCA 1195
Db 1137 CAGGTGACCCACCTGCTCAGCTTCCAAAGTGTGGGATTACAGGCTGGACACCTCA 1194
QY 1196 CCAGCGGCTATTTATGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1255
Db 1195 CCAGCGGCTATTTATGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1254
QY 1256 AGGCTGTCTCAAACTTGTGCTTCAATGCAATCTTCCAAATGAGGCAACACCCAGCC 1315
Db 1255 AGGCTGTCTCAAACTTGTGCTTCAATGCAATCTTCCAAATGAGGCAACACCCAGCC 1314
QY 1316 AGTCACATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1375
Db 1315 AGTCACATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1373
QY 1376 CATGTCAAACTGCAAAATTCAGTAGTAACAGAGTCTTT 1414
Db 1374 ATGCGGCAACCTGCAAAATTCAGTAGTAACAGAGTCTTT 1412

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## RESULT 5

US-09-964-412-4  
Sequence 4, Application US/09964412  
Patent No. US20020129391A1

## GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

Wands, Jack R.

TITLE OF INVENTION: Transgenic Animals and Cell Lines for

Screening Drugs Effective for the Treatment or Prevention of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/964.412

FILING DATE: 28-Sep-2001

CLASSIFICATION: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Esmoud, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0609.4370000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1418 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-964-412-4

Query Match 84.8%; Score 1223.4; DB 10; Length 1418;  
Best Local Similarity 96.9%; Pred. No. 3.5e-247;  
Matches 1375; Conservative 0; Mismatches 31; Indels 13; Gaps 12;

Db 1 TTTT... 60  
Qy 62 CTCAC... 121  
Db 61 CTCAC... 120  
Qy 122 AGTA... 180  
Db 121 AGTA... 179  
Qy 181 TAGAG... 240  
Db 180 TAGAG... 238  
Qy 241 CTC... 298  
Db 239 CTC... 298  
Qy 300 CTC... 359  
Db 299 CTC... 358  
Qy 360 CTC... 419  
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Db 898 CTC... 957  
Qy 956 CTC... 1015  
Db 958 CTC... 1017  
Qy 1016 CTC... 1075  
Db 1018 CTC... 1076  
Qy 1076 CTC... 1135  
Db 1077 CTC... 1136

Qy 1136 CAGT... 1195  
Db 1137 CAGT... 1194  
Qy 1196 CAGT... 1255  
Db 1195 CAGT... 1254  
Qy 1256 CAGT... 1315  
Db 1255 CAGT... 1314  
Qy 1316 CAGT... 1375  
Db 1315 CAGT... 1373  
Qy 1376 CAGT... 1414  
Db 1374 CAGT... 1412

RESULT 6  
US-09-964-666-3  
Sequence 3, Application US/09964666  
Patent No. US20020104108A1  
GENERAL INFORMATION:  
APPLICANT: de la Monte, Suzanne  
Mands, Jack R.  
TITLE OF INVENTION: Transgenic Animals and Cell Lines for  
Screening Drugs Effective for the Treatment or Prevention  
of Alzheimer's Disease  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
STERNE, Kessler, Goldstein & Fox, P.L.L.C.  
STREET: 1100 New York Ave., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/964,666  
FILING DATE: 28-Sep-2001  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 0609,4370000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2540  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1381 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-964-666-3  
Query Match  
Best Local Similarity 74.9%; Score 1080.2; DB 10; Length 1381;  
Matches 1317; Conservative 0; Mismatches 53; Indels 25; Gaps 18;





OY	244	CCGTCGTGGCGCTCCCAAAAGTCTCTGATCTACAGACTGGGCACCATTGCCGCGCTCGCCTGG	303
Dd	39758	CCACCTTG6CCTCCCAAAGTCT- GGGATTACAGGTGTGAATTTTACAAGAAAACATTTA	39700
OY	304	CTAATTTTTTGTGAGAACAAGGTTTCACTGATGTGCCAAGCTGTCTCTGTAGCTCA	363
Dd	39699	AGTATGAAGAAGCATACCTCCGGAAATATCACAGGCGCCTCCAACCCAGCCTCGAAGACTC	39640
OY	364	AGCAGTCCACCTGCTCTAGCCTCCCAAGTGTGGGATTA-----	403
Dd	39639	TTCACCTTGCTCTGTGGTGGGCCACACCTACCTCCACCTAAACTGGGCTGTGTCTTT	39580
OY	404	CAGGCGTGCACGCGCTGGCGCTCTATTTATTTATTTTAAAGACACAGCTGTCCCAC	463
Dd	39579	CCCCCTCCATCCCGCCTTTTTTTTTTTTTTTTTTTTTTTTGTGACAGAGTCTGTGTT	39520
OY	464	TCTTACCAGAGTAGAGTGACAGTGTGTGATCAGCTACGCTACGACCTTCAACTCTGA	523
Dd	39519	TGTTGCCAGAGCTGAGTGCAGTGTGTGCAAACTGTGCACAGCGCCTGTGATCTTTGG	39460
OY	524	GATC -AACCATCTCTCTCTCCAGCTCCCAAGTAGTGTGGGGCCAAAGCATAGCACACT	582
Dd	39459	GCTCAAGAGATCTCTCCACCTCAGCCTCTGTAGTAGTGTGGACTATAGTGTATGCTCAC	39400
OY	583	ACACCTGGCTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	642
Dd	39399	ATGCCACCTAATTTTTTTTTT-----TTTTTGAAGATGGAGTTTCGCTCTTTTGG	39348
OY	643	CCCAGCGTGGAGTGCAGTGGGCGCATCTTGGCTACTGCAACCTGTGCTCCGGGTTCA	702
Dd	39347	CCCAGCGTGGGTTGGAATGTGGTGCATGTGGCTACTGTCAACCTGTGCTCCGGGTTCA	39288
OY	703	AGTTATCTCTGCCCCAGCCTCTCGAGTAGCTGGAGCATACAGGCGCCACCACCCCTAG	762
Dd	39287	AGCATTTCTCCGCTCAACCCCCAGTAGTGGGATTCAGGATGCGCATATCACACC	39228
OY	763	CTAATTTTTTGTATTTTATAGTAGAGATGGG - TTCACCATGTTCGCCAGGTYTATCTTG	821
Dd	39227	TGGCTAATTTTGTATTTTATAGTAGAGATGGGTTTCACTATGTCACTAGCTGATTTCTCA	39168
OY	822	ATCTCTGAGACT - TGTATCTGCTGCTGCGCTGCCCTCCCAAGTCTGGGATTTACAGCG	879
Dd	39167	AACCTCTGACCTCAGAGATCTCTCTGCTGGCCTCCCAAGGCGTGGGATTTACAGGTG	39108
OY	880	TGAGCCACACGCGCCGCTT - ATTTTATTTTTTGTGTTGAATGGAATCTCATC	937
Dd	39107	TGAGCCACCTGTGCTGGGCTGTGCAATTTTTTTTTTTTTTTTTTTTGTGAGACAAGCTCTGC	39048
OY	938	TGTTACCCAGGCTGGAGTGCATGTGCAAAATCTGGCTACTAGCAACCTCTGCTCCGG	997
Dd	39047	TCTTTCGCCAGCTGGAGTGTGATGTCACCACTCGGCTACTGTGCAACCTCTGCTTTTGG	38988
OY	998	GCTCAGGCAATCTCTGTCTCAGGCTCTCCCAAGCAGCTGTGGATACGGGCACTGTGCACC	1057
Dd	38987	GTTCAAGCAATTTCTCTGCTCAGTCTCCCAAGTAGCTAGCTAGCAAGCAATGTGCACC	38928
OY	1058	ACACCCGCTAATTTTGTATTTTATTTAATAGAGCGGGGTTTACATAATTTGTACGGCTG	1117
Dd	38927	ACGCCGGCTAATTTTGTATTTTATTTTATTTAGTAGAACAAGGTTTACCATGTTGGCCACATG	38868
OY	1118	GTTCAAACTCTGACTAGTGTGACCCACTGTGCTCAGCCTTCCAAAGTGTGGGATTA	1177
Dd	38867	GTTCTGAATCTCTAATCTCAGGTGATCCACCGGCTCTGCTCCCAAATGTGGGATTA	38808
OY	1178	CAGCGGTGACCACTCACCCAGCC--- GCCTAATTTGATAAAAAATATGTACAT	1233
Dd	38807	CAGGCATGAGCCACACACACTGCTGCTGCCAATCTAATTAATAAAATTTTTGTAGAG	38748
OY	1234	GGGGGCTCTCTGATTTTCCAGGCTGTCTCAAACTCTGGCTCAAGCATCTCTCC	1293
Dd	38747	ACAGATCTCAGATATGTTTCCAGACTGTGCTTTGAACCTCTGGGCTTAAGGATGTCTCT	38688
OY	1294	AAATGAGCCAC 1304	

Db	38687	GTCTCAGCCTC	38677
RESULT 9			
US-09-962-436-292/c			
Sequence 292, Application US/09962436			
Patent No. US20020081301A1			
GENERAL INFORMATION:			
APPLICANT: Soppet, Daniel			
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign			
TITLE OF INVENTION: Sets			
FILE REFERENCE: 689290-75			
CURRENT APPLICATION NUMBER: US/09/962,436			
CURRENT FILING DATE: 2001-09-25			
PRIOR APPLICATION NUMBER: US/60/235,082			
PRIOR FILING DATE: 2000-09-25			
PRIOR APPLICATION NUMBER: US/60/234,924			
PRIOR FILING DATE: 2000-09-25			
NUMBER OF SEQ ID NOS: 568			
SOFTWARE: PatentIn version 3.0			
SEQ ID NO 292			
LENGTH: 65608			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURE:			
NAME/KEY: misc_feature			
OTHER INFORMATION: n=a,t,g or c			
US-09-962-436-292			
Query Match	40.8%	Score 587.8:	DB: 10; Length 65608;
Best Local Similarity	70.6%	Pred. No. 4.9e-114;	
Matches 940: Conservative	0;	Mismatches 347;	Indels 44; Gaps 10;
0Y	4	TTTTTTTGAGATGAGATTTTGGCTTGTGTCGCCAGGCGTGGAGTGCATAGGCGCATCT	63
Db	39993	TTTTTTTGAAGTAGAGTTT-GCTCTGTGGCCAGGCGTGAAGTATGATGCGACGATCT	39935
0Y	64	CAGCTACCGCAGCTCCGCGCTCCGGGTTCAAGGATTTCTCTCGCTCAGCTCCAG	123
Db	39934	CAGCTACCGCAGCTCCGCGCTCCGGGTTCAAGGATTTCTCTCGCTCAGCTCCAG	39875
0Y	124	TAGCTGGGATTCAGAGCATGTGCACCCAGCGCTGGCTAATTTTGAATTTTCTTAGTAG	183
Db	39874	TAGCTGGGATTCAGAGCATGTGCACCCAGCGCTGGCTAATTTTGAATTTTCTTAGTAG	39819
0Y	184	AGATGAGATTTCTCATGTGTGTCAGGCTGTCTGAACTCCGACCTCAGATGATCCT	243
Db	39818	AGATGAGATTTCTCATGTGTGTCAGGCTGTCTGAACTCCGACCTCAGATGATCCT	39759
0Y	244	CGCTCGGCGCTCCCAAGTGTCTAATACAGGACTGGCCACCATCCCGGCTCTGCTGG	303
Db	39758	CGCTCGGCGCTCCCAAGTGTCTAATACAGGACTGGCCACCATCCCGGCTCTGCTGG	39700
0Y	304	CTAATTTTGTGTGTAAGAAACAGGGTTTCACTGATGTGCCAAGCTGTGCTCAGCTCA	363
Db	39699	CTAATTTTGTGTGTAAGAAACAGGGTTTCACTGATGTGCCAAGCTGTGCTCAGCTCA	39640
0Y	364	AGCAGTCCACCTGCGCTCAGCTCCCAAGTGTGAGATTA-----	403
Db	39639	TTTACTTGTCTGGCTGGGCGCTCCACCTCAGCTCCCAAGTGTGAGATTA-----	39580
0Y	404	CAGGCTGGAGCGGCTCGGCGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	463
Db	39579	CCCCCTCATCCCTGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	39520
0Y	464	TCTTACCCAGATGAAGTCACTGTGTATCAGACCTACTGACGCTTCAACTCTGTA	523
Db	39519	TCTTACCCAGATGAAGTCACTGTGTATCAGACCTACTGACGCTTCAACTCTGTA	39460
0Y	524	GATTC-AAGATCTCTGCTGAGCTCCCAAGTACTGGAGCAAAAGCATGACGACT	582
Db	39459	GCTCAAGATCTCTGAGCTCCCAAGTACTGGAGCAAAAGCATGACGACT	39400





Db 39107 TGAGCCACTGTCGCTGAGCCTGCCAAATTTTTTTTTTTTTTTGGAGACAAAGTCTGCG 39048  
QY 938 TGTATCCAGGCTGGAGTGCATGSCAAATCTGGCTCAGTCAACCTGCTGCCG 997  
Db 39047 TCTTCCAGGCTGGAGTGCATGSCAAATCTGGCTCAGTCAACCTGCTGCCG 38988  
QY 998 GCTCAAGGATTTCTCTCTCTGAGCCTCCCAAGCAGTGGATTCAGGCGACCTCCAC 1057  
Db 38987 GTTCAAGGATTTCTCTCTGCTCAGTCTCCCAAGTAGTCAAGCAGTGTGCGAC 38928  
QY 1058 ACACCCGCTAATTTTGTATTTTCAATAGAGCGGGTTTACCAATATTTTCAGGCTG 1117  
Db 38927 ACAGGCTGATTTTGTATTTTGTAGTGAAGACAGTGTTCACATGTGTGCGACGACTG 38868  
QY 1118 GTCCTCAACTCTGACCTGAGTGCACCACTGCTGACCTTCCAAATGTGGGATTA 1177  
Db 38867 GCTTGAACCTCTTAACCTCAGTGTATCCACCGCTCTGCTCCCAAGTGTGGGATTA 38808  
QY 1178 CAGGCGTAGCCACCTCAACCCAGCC---GGCTAATTTAGATAAAAAATATGTAGCAAT 1233  
Db 38807 CAGGATGAGCCACACACCTGCTGCTGCTGCTCAATTAATAAATTTTGTAGAG 38748  
QY 1234 GGGGCTCTGCTATGTTGCTCCAGGCTGCTCAACCTTCTGCTTCAATGCAATCTTCC 1293  
Db 38747 ACAGATCTCACTATGTGTCCAGACTGTCTTGAACCTCTGCTTAAAGGATCTCTCT 38688  
QY 1294 AATGAGCCAC 1304  
Db 38687 GCTCAGGCTC 38677

RESULT 11  
US-09-954-456-2257

Sequence 2257. Application US/09954456  
Patent No. US20020115057A1  
GENERAL INFORMATION:  
APPLICANT: Young, Paul  
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Can  
FILE OF INVENTION: Sets  
FILE REFERENCE: 689290-76  
CURRENT APPLICATION NUMBER: US/09/954,456  
CURRENT FILING DATE: 2001-09-18  
PRIOR APPLICATION NUMBER: US/60/233,617  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: US/60/234,052  
PRIOR FILING DATE: 2000-09-20  
PRIOR APPLICATION NUMBER: US/60/234,923  
PRIOR FILING DATE: 2000-09-25  
PRIOR APPLICATION NUMBER: US/60/235,134  
PRIOR FILING DATE: 2000-09-25  
PRIOR APPLICATION NUMBER: US/60/235,637  
PRIOR FILING DATE: 2000-09-26  
PRIOR APPLICATION NUMBER: US/60/235,638  
PRIOR FILING DATE: 2000-09-26  
PRIOR APPLICATION NUMBER: US/60/235,711  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: US/60/235,720  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: US/60/235,840  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: US/60/235,863  
PRIOR FILING DATE: 2000-09-27  
NUMBER OF SEQ ID NOS: 2276  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2257  
LENGTH: 62944  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-954-456-2257

Query Match 36.4%; Score 524.4; DB 10; Length 62944;  
Best Local Similarity 71.9%; Pred. No. 8,6e-101;  
Matches 963; Conservative 0; Mismatches 321; Indels 56; Gaps 19;

QY 1 TTTTATTTTATGATGAGTATTTTTCCTGTGTGCCAGGCTGAGTCAATGGCGCA 60  
Db 59357 TATTTATTTTATGATGAGTATTTT-CTCTTCTGCGCCAGGCTGAGTCAATGGCGCA 59415  
QY 61 TCTCAGCTCAGCGCAACCTCCGCTCCCGGTTCAAGCATTCCTGCTCAGCTCC 120  
Db 59416 TCTGCTCAGTCAACCTCCGCTCCCTGATTAATTAATTAATTCCTGCTCAGCT--- 59472  
QY 121 CAGTACCTGGGATTTACAGCATGTGACCCAGGCTGGCTAATTTTGTATTTTATG 180  
Db 59473 TAGTACGTGTGATTTACAGCATGTGACCCAGGCTGATTAATTTT---TGTATTTTAC 59529  
QY 181 TAGAGTATGATTTTTCATTTTGTGTCAGGCTGTGTCACATCCGACCTCAGATATC 240  
Db 59530 TAGAGTATGATTTTTCATTTTGTGTCAGGCTGTGTCACATCCGATTTAGTTATC 59589  
QY 241 CCTCGCTGCGCTCCCAAGTCTAG---ATACAGGATGCGCACCATGCGCGCTC 296  
Db 59590 TGCCTACCTGCGCTCCCAAGTCTGAGTATACACAGTGAAGCCACGACCCAGCTC 59649  
QY 297 TGCCTGCTAAT-TTTTGTGTAAGAACAGGCTTTCAGTATGTGCCAAGCTGTCTC 355  
Db 59650 TTTTCTTTTCTTTTCTTTTCTGAGCAGGCTGTGCTGTGTCACCCAGGCTGAGTGC 59709  
QY 356 TG---AGCTCAAGCAGTCCACCTGACCTGACCTCCCAAGTCTGGATTTACAGGCTG 411  
Db 59710 AGCAGAGGATCATACCTCAGTCTGATCTCCGCTGTCACATGATTCCTCCAGCT 59769  
QY 412 CAGCGCTGCTGCGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 471  
Db 59770 AATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 59828  
QY 472 AGATTAAGTGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 531  
Db 59829 AGACTGAGTGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 59887  
QY 532 ATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 591  
Db 59888 AATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 59946  
QY 592 TAAATTTTAA-TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 649  
Db 59947 TAAATTTTGGGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 60005  
QY 650 TGGAGTGAAGTGGGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 709  
Db 60006 TGGAGTGAAGTGGGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60065  
QY 710 CTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 759  
Db 60066 CTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60125  
QY 760 TACGTAAAT---TTTGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 815  
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QY 816 ATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 875  
Db 60186 GTCTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60245  
QY 876 GGGGTGAGCCACGACGCGGCTTAAT-----TTTAAATTTTGTGTTTGAAT 925  
Db 60246 GGGTTAGGAGACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60305  
QY 926 GGAATCTCACTGTATCCAGGCTGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGA 965  
Db 60306 GAATTTTGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60365  
QY 986 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1045  
Db 60366 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60425





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Db 19073 AGCCCGGCTGCTTGGCTCCCAAGTGTAGATTTACAGCATGAGCCACCAAGCCCTG 19132
QY 294 CTGCGCTGGCTAATTTTGTGGTGAAGAAACAGGGTTTCACTGATGTCGCAAGCTGTCT 353
Db 19133 ACCT-----TTTTTTTTTTTTTGGAGAGAGCTCTGTTTGTACACCGAGCTGGAGT 19185
QY 354 CCTG-----AGCTCAGCAGTCCACCTGCTCAGCTCCCAAAATGCTGGATTAACAGC 408
Db 19186 GCAGTGGCAGCATCTGGCTCAGTCAAGCTCTGCTCCAGGTTCAATGCTCTCTCTG 19245
QY 409 GTGAGCCGCTGCTGCTTATTTATTTTATTTTAAAGCAGAGTGTCCCACTCTTA 468
Db 19246 CCTCAGGCTCCCAAGTAGTGGGAGTACAGCACTTCCACAGCCGCGGTATTTT 19305
QY 469 CCCAGATGAGTGTGATGATCAGCT---CAGTCAGCCCTTCAACTCTCTAGA 525
Db 19306 GTATTTTATAGATAGGAGTTTCAACCGTTAGCCAGATGCTGTGATTTCTGACC 19365
QY 526 TCAAGATCTCTGCTCAGCTCCCAAGTACCTGGGAGCAAGATGATCAGCACTACA 585
Db 19366 TCGTG-ATCCACTCTGCTTGGCTCCCAAGTGTGATTAAGCGTGTGAGCCACCTG 19424
QY 586 CCGGCTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 19480
Db 19425 CCCGGC---CTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 19540
QY 646 AGGCTGAGTGTGAGTGGCAATCTTGGCTCAGTCACTGCTGCTGCTGCTGCTGCTGCT 705
Db 19481 AGGCTGAGTGTGAGTGGCTGATTAACAGTCACTGAGCTCAATCTCTGAGTCAAGC 19540
QY 706 TATTCCTGCTCCCAAGCTCCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 762
Db 19541 AATCTCTCAGCTCAGCTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 19600
QY 763 CTAATTTTGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 822
Db 19601 ATATTTTGTGCTTTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 19660
QY 823 TCTGTGAC-CTTGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 881
Db 19661 TTCTGGGCTCAAGTATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19720
QY 882 AGCCACAGCCCGGCTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 941
Db 19721 TGCATGTGTCACCAAGATATGATTTTCTTTTTCAGAGGGGTCTCACTCTGTT 19780
QY 942 ACCAGGCTGAGTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1001
Db 19781 GCCAGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 19840
QY 1002 AAGCAGTCTGCTGCTCAGCTCCCAAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1061
Db 19841 AAGCAGTCTGCTGCTCAGCTCCCAAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 19900
QY 1062 CCCGCTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1121
Db 19901 CCGGCTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 19960
QY 1122 CAACTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1181
Db 19961 CAACTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 20020
QY 1182 CGTGAGCCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1225
Db 20021 CATGAGCCATTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 20064

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RESULT 15  
 US-09-918-686-1  
 ; Sequence 1, Application US/09918686  
 ; Patent No. US20020076720A1  
 ; GENERAL INFORMATION:

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; APPLICANT: Brunkov, Mary
; APPLICANT: Proill, Sean
; APPLICANT: Paepel, Bryan
; APPLICANT: Staehling-Hampton, Karen
; TITLE OF INVENTION: METHODS FOR IDENTIFYING
; FILE REFERENCE: 240083.515
; CURRENT APPLICATION NUMBER: US/09/918.686
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 92139
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7043, 8369, 8401
; OTHER INFORMATION: n = A,T,C or G
US-09-918-686-1

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Query Match 33.2%; Score 479.2; DB 10; Length 92139;  
 Best Local Similarity 68.3%; Pred. No. 2,6e-91;  
 Matches 850; Conservative 0; Mismatches 358; Indels 36; Gaps 12;

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Search completed: February 1, 2003, 23:51:03  
 Job time : 432 secs





GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 21:20:53 ; Search time 66 Seconds  
(without alignments)  
6700.423 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 441362 segs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

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6: /cgn2\_6/prodata/2/ina/backfilesl.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1442	100.0	1442	2	US-08-450-673C-120
4	1442	100.0	1442	2	PCT-US95-17111A-120
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6	1080.2	74.9	1381	2	US-08-340-426D-49
7	1080.2	74.9	1381	2	US-08-450-673C-49
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29	370	25.7	4793	4	US-09-561-497-10	Sequence 10, Appl
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ALIGNMENTS

RESULT 1  
US-08-454-557C-120  
; Sequence 120, Application US/08454557C  
; Patent No. 5830670  
; GENERAL INFORMATION:  
; APPLICANT: de la Monte, Suzanne  
; TITLE OF INVENTION: Neutral Thread Protein Gene Expression and Detection  
; TITLE OF INVENTION: Of Alzheimer's Disease  
; NUMBER OF SEQUENCES: 121  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/454,557C  
; FILING DATE: 30-MAY-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ludwig, Steven R.  
; REGISTRATION NUMBER: 36,203  
; REFERENCE/DOCKET NUMBER: 0609,3840003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2540  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 120:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1442 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: both  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 15..1139  
; US-08-454-557C-120  
Query Match 100.0%; Score 1442; DB 2; Length 1442;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1442; Conservative 0; Mismatches 0; Gaps 0;  
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RESULT 2  
US-08-340-426D-120  
; Sequence 120, Application US/08340426D  
; Patent No. 5948634  
; GENERAL INFORMATION:  
; APPLICANT: de la Monte, Suzanne  
; TITLE OF INVENTION: Neutral Thread Protein Gene Expression and Detection  
; NUMBER OF SEQUENCES: 121  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/340,426D  
; FILING DATE: 14-NOV-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ludwig, Steven R.  
; REGISTRATION NUMBER: 36,203  
; REFERENCE/DOCKET NUMBER: 0609,3840002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 120:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1442 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: both  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 15..1139  
; US-08-340-426D-120

Query Match

100.0%; Score 1442; DB 2; Length 1442;

Best Local Similarity	100.0%	Pred No. 0	
Matches 1442; Conservative	0	Mismatches	0
		Indels	0
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QY	1261	GGTCTCAAACTTTGGGCTTATGCAATCCCTCCAAATGAGCCACAACCCAGCCAGTCA	1320
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Db	1441	CA 1442	

RESULT 3  
US-08-450-673C-120

; Sequence 120, Application US/084506/3a  
; Patent No. 5948888

GENERAL INFORMATION

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

APPLICANT: Wands, Jack R.

TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection

TITLE OF INVENTION: of Alzheimer's Disease

NUMBER OF SEQUENCES: 121

NUMBER OF SEQUENCES: 121  
CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:  
stern Kessler, Goldstein &

ADDRESSEE: Sterne, Kessler, Goldstein &  
100 New York Avenue, Suite 600

STREET: 1100 New

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

COUNT: 0.0000  
ZTP: 20005-3934

ZIP: 20003-3334  
COMPUTER READABLE FORM:

COMPUTER READABLE FORM.  
MEDIUM TYPE: Floppy disk

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;
MEDIUM TYPE: floppy disk
CONVERTED: IBM PC compatible

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COMPUTER: IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, V
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/0

FILED DATE: 30-MAY-1995

CLASSIFICATION: 530

CLASSIFICATION: 250  
ATTORNEY/AGENT INFORMATION:

ATTORNEY/AGENCY INFORMATION:  
NAME: Judith Steven R.

NAME: Ludwig, Steven R.  
REGISTRATION NUMBER: 36,203

REGISTRATION NUMBER: 36,200  
REFERENCE / DOCKET NUMBER: 06

REFERENCE/DOCKET NUMBER: 06

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2

INFORMATION FOR SEQ ID NO

SEQUENCE CHARACTERISTIC

SEQUENCE CHARACTERISTICS

LENGTH: 1442 base  
TYPE: nucleic aci

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;
TYPE: nucleic acid
SET: unknown; double

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NAME/KEY: CDS ;

LOCATION: 15..1139  
US-08-450-673C-120

Query Match	100.0%;	Score 1442;	DB 2;	Length 1442;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1442; Conservative	0;	Mismatches	0;	Twofold

Oy	1	TTTTTTTTTTTGGAGATGGAGTTTTCGCTTGTGTCGCCAGGCTGGAGTGCATATGGCGCA	60
Db	1	TTTTTTTTTTTGGAGATGGAGTTTTCGCTTGTGTCGCCAGGCTGGAGTGCATATGGCGCA	60
Oy	61	TCTCAGCTCACCGCAACCTCCGGCCCGCGGGTTCAAGCGATTCTCTGCTCAGCTCCC	120
Db	61	TCTCAGCTCACCGCAACCTCCGGCTCCGGTTCAAGCGATTCTCTGCTCAGCTCCC	120
Oy	121	CAGTACGTGGGATTACAGGATGTGACCCACGCTGGGCTAAATTTGATTTTTTTAG	180
Db	121	CAGTACGTGGGATTACAGGATGTGACCCACGCTGGGCTAAATTTGATTTTTTTAG	180
Oy	181	TAGAGATGGAGTTTCTCCATGTGGTGTGACGCTGCTCTGCAACTCCGACCTCAGATATC	240
Db	181	TAGAGATGGAGTTTCTCTCATTGTTGGTGTGACGCTGCTCTGCAACTCCGACCTCAGATATC	240
Oy	241	CCCTCCGCTTCGGGCTCCCAAAAGTCTAGATACAGAGCTGGCCACCATGGCCGGCTCTGCC	300
Db	241	CCCTCCGCTTCGGGCTCCCAAAAGTCTAGATACAGAGCTGGCCACCATGGCCGGCTCTGCC	300
Oy	301	TGGCTAAATTTTGTGGTACGAACAGGGTTTCACTGATGTGCCCCAAGCTGGTCTCTGAGC	360
Db	301	TGGCTAAATTTTGTGGTACGAACAGGGTTTCACTGATGTGCCCCAAGCTGGTCTCTGAGC	360
Oy	361	TCACAGCATCCACCTGCTCAGCCCTCCAAAGTGTGGGATTACAGGCGTGGACCGCTGC	420
Db	361	TCACAGCATCCACCTGCTCAGCCCTCCAAAGTGTGGGATTACAGGCGTGGACCGCTGC	420
Oy	421	CTGGGCTTTTATTTTATTTTATTTTAAAGCAGAGGTGTCCACTTTTACCAGAGTGAAG	480
Db	421	CTGGGCTTTTATTTTATTTTATTTTAAAGCAGAGGTGTCCACTTTTACCAGAGTGAAG	480
Oy	481	TGCAAGTGGTGTGATCAGAGCTCAGAGCTTCAACTCTGTAGATCAAGCAATCCCTCGT	540
Db	481	TGCAAGTGGTGTGATCAGAGCTCAGAGCTTCAACTCTGTAGATCAAGCAATCCCTCGT	540
Oy	541	CCCTCAGCTCCCAAGTACCTGGGAGCCAAAGACATGTACACCTTACACCTGGCTAATTTTAA	600
Db	541	CCCTCAGCTCCCAAGTACCTGGGAGCCAAAGACATGTACACCTTACACCTGGCTAATTTTAA	600
Oy	601	TTTTTATTTTAAATTTTGTGACAGAGTCTCACTGTCTACCCAGGCTGGAGTGCAGT	660
Db	601	TTTTTATTTTAAATTTTGTGACAGAGTCTCACTGTCTACCCAGGCTGGAGTGCAGT	660
Oy	661	GGGCAATCTTGGCTCACTGCAACCTGTGCTCCCGGGTTCAGTTATTCCTGCCCCA	720
Db	661	GGGCAATCTTGGCTCACTGCAACCTGTGCTCCCGGGTTCAGTTATTCCTGCCCCA	720
Oy	721	GGCTCTGAGTACTGGGACTACAGCGCCACACAGCTAGCTAATTTTGTGATTTT	780
Db	721	GGCTCTGAGTACTGGGACTACAGCGCCACACAGCTAGCTAATTTTGTGATTTT	780
Oy	781	TAGTAGAGATGGGTTCCACCATGTGTGCCAGGTGATCTTGATCTGTGACCTGTGATC	840
Db	781	TAGTAGAGATGGGTTCCACCATGTGTGCCAGGTGATCTTGATCTGTGACCTGTGATC	840
Oy	841	TGGCGGCTCGGCTCCCAAAAGTGTGGGATTACAGAGCTTGAGCCACACCGCCGGGCTTA	900
Db	841	TGGCGGCTCGGCTCCCAAAAGTGTGGGATTACAGAGCTTGAGCCACACCGCCGGGCTTA	900
Oy	901	TTTTTAAATTTTGTGTTTGAANAAGGAATCTCATCTGTTCACCAAGCTGGAGTGCAT	960
Db	901	TTTTTAAATTTTGTGTTTGAANAAGGAATCTCATCTGTTCACCAAGCTGGAGTGCAT	960
Oy	961	GGCCAAATCTGGGCTACATGCACCTGTGCTCCCGGGCTCAAGGATTTCTCTGTCA	1020
	4		

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Db      961  GGCCAAATCTCGGCTCACTGCAACACTCTGCTCCGCCGCGCTCAAGCGAATTCCTCTGTCTCA  1020
QY      1021  GCTCTCCACAGCACTGGGATTAACGGGACACTGCGACACACACCCGGCTAATTTTGTATTT  1080
Db      1021  GCTCTCCAAACACACTGGGATTAACGGGACACTGCGACACACACCCGGCTAATTTTGTATTT  1080
QY      1081  TCATTAGAGGCGGGGTTTGCACATATTTGTCAAGCTGGTCTCAAACTGCTGACCTCAGGT  1140
Db      1081  TCATTAGAGGCGGGGTTTGCACATATTTGTCAAGCTGGTCTCAAACTGCTGACCTCAGGT  1140
QY      1141  GACCCACCTGCTCAGGCTTCCAAAGTCTGTGGATTACAGGCGTAGAGCAACCTCACCCAG  1200
Db      1141  GACCCACCTGCTCAGGCTTCCAAAGTCTGTGGATTACAGGCGTAGAGCAACCTCACCCAG  1200
QY      1201  CCGGCAATTTTGATTAATAAATAATGTAGCAATGGGGGGTCTTGCTATGTTGGCCAGGCT  1260
Db      1201  CCGGCAATTTTGATTAATAAATAATGTAGCAATGGGGGGTCTTGCTATGTTGGCCAGGCT  1260
QY      1261  GGTCTCAAACTTGTGGCTTCATGCAATCTTCCAAATAGAGCGCAACACCCAGCAGTCA  1320
Db      1261  GGTCTCAAACTTGTGGCTTCATGCAATCTTCCAAATAGAGCGCAACACCCAGCAGTCA  1320
QY      1321  CATTTTAAACAGTTATCATCTTATTTATTTAGTATCTAGAAATTAACATTAACATGT  1380
Db      1321  CATTTTAAACAGTTATCATCTTATTTATTTAGTATCTAGAAATTAACATTAACATGT  1380
QY      1381  CAAACGTGCAAAATTCAGTAGTAACAGAGTCTTTTAATCTTTAAACAAACCTTTAGAG  1440
Db      1381  CAAACGTGCAAAATTCAGTAGTAACAGAGTCTTTTAATCTTTAAACAAACCTTTAGAG  1440
QY      1441  CA 1442
Db      1441  CA 1442

RESULT 4
PCT-US95-17111A-120
? Sequence 120, Application PC/TUS9517111A
? GENERAL INFORMATION:
? APPLICANT: de la Monte, Suzanne
? APPLICANT: Wands, Jack R.
? TITLE OF INVENTION: Neutral Thread Protein Gene Expression and
? TITLE OF INVENTION: Detection of Alzheimer's Disease
? NUMBER OF SEQUENCES: 121
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
? STREET: 1100 New York Avenue, Suite 600
? CITY: Washington
? STATE: D.C.
? COUNTRY: U.S.A.
? ZIP: 20005-3934
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent In Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: PCT/US95/17111A
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/340,426
? FILING DATE: 14-NOV-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Ludwig, Steven R.
? REGISTRATION NUMBER: 36,203
? REFERENCE/DOCKET NUMBER: 0609.3840002
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202) 371-2600
? TELEFAX: (202) 371-2540
? INFORMATION FOR SEQ ID NO: 120:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1418 base pairs

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OY	2	TTTTTTTTTTTGAAGATGAGATTTCGCTCTGTGTGGCCAGAGCTGGAGTGCMAATGGCCAAAT	61
Db	1	TTTTTTTTTTTGAAGATGAGATTTCGCTCTGTGTGGCCAGAGCTGGAGTGCMAATGGCCAAAT	60
OY	62	CTGAGCTCAACCGCAACCTCCGCGCTCCGGGTTCAAGGATTTCTCCGCTCAACCTCCGC	12
Db	61	CTGAGCTCAACCGCAACCTCCGCGCTCCGGGTTCAAGGATTTCTCCGCTCAACCTCCGC	12
OY	122	AGTACTGGGATTTACAGCATGTGACACCACAGCTCGGCTAATTTTATTTTTTTTAACT	18
Db	121	AGTACTGGGATTTACAGCATGTGGA-CCAGCTCGGCTAATTTTATTTTTTTTAACT	17
OY	182	AGAGATGAGGATTT--CTGCATGTTGTGACGGTGTGTGMACTCCGCACTCAGATGAT	23
Db	180	AGAGATGAGGATTTAACTCATGTTGTGTGACGGTGTGTGMACTCCGCACTCAGATGAT	23
OY	240	CCCTCGCTCTGGGCTCCCAAGTGT--AGATPACAGATCTGGCCACCATGCCCCG-CT	29
Db	240	CTCCCGTCTCGGCTCGCCCAAGTGTGAGATTACAGGATTAAGGACACCATGCCCCGCT	29
OY	296	CTGCGCTCAATTTTTTGTGTGAAACAGGGTTTCACTGATG-TGCCCAAGTGGTCTC	35
Db	300	CTGCGTGGCTAATTTTTTGTGTGAAACAGGGTTTCACTGATGTTGCCCAAGTGGTCTC	35
OY	355	CTGAGCTCAACAGTCCACCTGCGCTCAGGCTCCCAAGTGTGGGATTTACAGGGTGCAG	41
Db	360	CTGAGCTCAACAGTCCACCTGCGCTCAGGCTCCCAAGTGTGGGATTTACAGGGCT-CAG	41
OY	415	CCGAGCGCGGCTTTTTTATTTTATTTTTTTTAAACACAGGTGTGCCACTTAAACCAG	47
Db	419	CCGAGCGGCTTTTTTATTTTATTTTATTTTTTTTAAACACAGGTGTACCACCTTAAACCAG	47
OY	475	ATGAAGTCAAGTGTGTGATTCACAGCTCACTGACGCTTCAACTCTGAGATCAAG-AT	53
Db	479	ATGAAGTCAAGTGTGTGATTCACAGCTCACTGACGCTTCAACTCTGAGATCAAGCAAT	53
OY	534	CCGCTGCTCAAGCTCCCAAGTACTGGGACCAAAAGATGACCACTAACCTGCTGA	59
Db	539	CCGCTGCTCAAGCTCCCAAGTACTGGGACCAAAAGATGACCACTAACCTGCTGA	59
OY	594	AATTTATTTTATTTTATTTTATTTTTTTTGAAGACAGTCTCAACTCTGACCCAGGCTGA	65
Db	598	AATTTATTTTATTTTATTTTATTTTTTTTGAAGACAGTCTC-ACHTGTCACCCAGGCTGA	65
OY	654	GTCAGTGGCGCAATCTTGCTCACTCAACCTGTGCTCCGGGTTCAAGTATTTCTC	71
Db	657	GTCAGTGGCGCAATCTTGCTCACTCAACCTGTGCTCCGGGTTCAAGTATTTCTC	71
OY	714	TGCCACGCTCCGAGTACGTGGGACTACAGGCGCCACAGCGCTTACGATTTT	77
Db	717	TGCCACGCTCCGAGTACGTGGGACTACAGGCGCCACAGCGCTTACGATTTT	77
OY	774	GTAATTTTAAAGAGATGGGGTTCAACATGTGCGCAGGTTGATCTGTGAC	83
Db	777	GTAATTTTAAAGAGATGGGGTTCAACATGTGCGCAGGTTGATCTGTGAC	83
OY	833	TTTGAGATCTCGCTCGCGCT-CCCAAGTCTGGGATTTACAGGGGTAGGCACAC	89
Db	837	TTTGAGATCTCGCTCGCGCTCCGCGCTACCAAGTCTGGGATTTACG--GTGTACTCTCAG	89
OY	892	CCCGGCTAATTTTATTTTGTGTGAAATGGAATCTCACTGTGTACCCAGGCT	95
Db	895	CCCGGCTAATTTTATTTTGTGTGAAATGGAATCTCACTGTGTACCCAGGCT	95
OY	952	GAGTGCMAATGGCAATCTGCGCTCACTGCAACCTCGCTCCCGGCTCAAGCATCT	101

Db	955	GATGCAATG -CAATCTGGCTACTGCAACCTCTGCTCCCGGG -TCAAGCATTC	10112
Qy	1012	CGCTGTCAGCTCCCAAGCAGCTGGGATTAACGGGACCTGCGACCAACCCCGCTAAT	10711
Db	1013	CGCTGTCAGCTCCCAAGCAGCTGGGATTAACGGG -ACCTGACACACACCCCGCTAAT	10701
Qy	1072	TTTGTATTTTGAATAGAGGCGGGTTTCCACATATTTTGCAGCT -GGTCTCAAACTCT	11301
Db	1071	TTTGTATTTTCTATTAGAGCGGG -TTTACCATATTTTGCAGGCTGGGCTTCAAACTCT	11281
Qy	1131	GACCTCAGGTACCCACCCTGCTGAGCTTCCAAAGTGTGGGATTAACGCGTAGACCA	11301
Db	1129	GACCTCAGGTACCCACCCTGCTGAGCTTCCAAAGTGTGGGATTAACGCGTAGACCA	11301
Qy	1191	CTCACCAGCGGCGCTATTAGATTAATAAATAATATGTAGCAATGGGGGCTTGTCTATGT	12501
Db	1189	CTCACCAGCGGCGCTATTAGATTAATAAATAATATGTAGCAATGGGGG -TCTGCTATGT	12461
Qy	1251	TGCCAGGCGGTCTCAAACTTCTGGCTTCATGCAATCCCTCCAAATGAGCGCAACAC	13101
Db	1247	TGCCAGGCGGTCTCAAACTTCTGGCTTCATGCAATCCCTCCAAATGAGCGCAACAC	13061
Qy	1311	CAGCGATCACAATTTTAAACAGTTACATCTTAAATTTTAAATATCTAGTAAGAAATATACA	13701
Db	1307	CAGCGATCACAATTTTAAACAGTTACATCTTAAATTTTAACTAGTAAGAAATATACA	13661
Qy	1371	ATAAATCTGCAAC 1385	
Db	1367	ATAAATCTGCAAC 1381	

5-08-340-426D-49

US-08-340-426D-49





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QY 2 TTTTGTGAGATGAGATTTTCCTCTTGTGCCCAGGCTGAGTGCATGGCCGAT 61
   1 TTTTGTGAGATGAGATTTTCCTCTTGTGCCCAGGCTGAGTGCATGGCCGAT 60
Db 1 TTTTGTGAGATGAGATTTTCCTCTTGTGCCCAGGCTGAGTGCATGGCCGAT 60
QY 62 CTGAGCTACCGCAACCTCCGCTCCGCTTCACGCAATTCCTGCTCAGCTCC 121
   61 CTCAGCTACCGCAACCTCCGCTCCGCTTCACGCAATTCCTGCTCAGCTCC 120
QY 122 AGTACGCTGAGATTTACAGGCAATGACCCAGCTGCTGATTTTGTATTTT 181
   121 AGTACGCTGAGATTTACAGGCAATGACCCAGCTGCTGATTTTGTATTT 179
QY 182 AGAATGAGATTTTCTCATGTTGTGACGCTGCTGCTGCAACTCCGACCT 239
   180 AGAATGAGATTTTACATGTTGTGACGCTGCTGCTGCAACTCCGACCT 239
QY 240 CCGTCCGCTGCGGCTCCCAAGTGTCT--AGATACAGACGCGGACATGCC 295
   240 CTCCGCTGCGGCTCCCAAGTGTCTGAGATTTACAGGCAATGACCCAG 299
QY 296 CTGCTGCTGCTAATTTTGTGAGAACAGGTTTCACTGATG-TGCCAGCT 354
   300 CTGCTGCTGCTAATTTTGTGAGAACAGGTTTCACTGATGTTGCCAG 359
QY 355 CTGAGCTCAACGACGTCACCTGCTCAGCTCCCAAGTGTGAGATTTAC 414
   360 CTGAGCTCAACGACGTCACCTGCTCAGCTCCCAAGTGTGAGATTTAC 418
QY 415 CCGTCCGCTGCGGCTCCCAAGTGTCT--AGATACAGACGCGGACATGCC 474
   419 CCGTCCGCTGCGGCTCCCAAGTGTCTGAGATTTTAAAGCACAGGTTT 478
QY 475 ATGAGTGCAGTGTGTGATACAGCTCAGCTGCACTCTTCACTGAGATCA 533
   479 ATGAGTGCAGTGTGTGATACAGCTCAGCTGCACTCTTCACTGAGATCA 538
QY 534 CCGTCCGCTGCGGCTCCCAAGTGTCTGAGAACAGGTTTCACTGAGATCA 593
   539 CCGTCCGCTGCGGCTCCCAAGTGTCTGAGAACAGGTTTCACTGAGATCA 597
QY 594 ATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 653
   598 ATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 656
QY 654 GTGAGTGCAGTGTGTGATACAGCTCAGCTGCACTCTTCACTGAGATCA 713
   657 GTGAGTGCAGTGTGTGATACAGCTCAGCTGCACTCTTCACTGAGATCA 716
QY 714 TGCCAGCTGCTGAGTGTGATACAGCTGCACTCTTCACTGAGATCA 773
   717 TGCCAGCTGCTGAGTGTGATACAGCTGCACTCTTCACTGAGATCA 776
QY 774 GTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 832
   777 GTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 836
QY 833 TGTGATGCTGCGGCTCCGCTCCGCTTCACGCAATTCCTGCTCAGCTCC 891
   837 TGTGATGCTGCGGCTCCGCTCCGCTTCACGCAATTCCTGCTCAGCTCC 894
QY 892 CCGGCTGCTGAGTGTGATACAGCTGCACTCTTCACTGAGATCA 951
   895 CCGGCTGCTGAGTGTGATACAGCTGCACTCTTCACTGAGATCA 954
QY 952 GAGTGCATGAGCAATTCCTGCTCAGCTGCACTCTTCACTGAGATCA 1011
   955 GAGTGCATGAGCAATTCCTGCTCAGCTGCACTCTTCACTGAGATCA 1012
QY 1012 CCGTCCGCTGCGGCTCCCAAGTGTCT--AGATACAGACGCGGACATGCC 1071
   1013 CCGTCCGCTGCGGCTCCCAAGTGTCT--AGATACAGACGCGGACATGCC 1070
QY 1072 TTTTGTGAGATGAGATTTTCCTCTTGTGCCCAGGCTGAGTGCATGGCCGAT 1130

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Db 1071 TTTTGTGAGATGAGATTTTCCTCTTGTGCCCAGGCTGAGTGCATGGCCGAT 1128
QY 1131 GACCTCAGTGCAGTGTGATACAGCTGCACTCTTCACTGAGATCA 1190
   1129 GACCTCAGTGCAGTGTGATACAGCTGCACTCTTCACTGAGATCA 1188
QY 1191 CCGTCCGCTGCGGCTCCCAAGTGTCT--AGATACAGACGCGGACATGCC 1250
   1189 CCGTCCGCTGCGGCTCCCAAGTGTCT--AGATACAGACGCGGACATGCC 1246
QY 1251 TGCCAGCTGCTGAGTGTGATACAGCTGCACTCTTCACTGAGATCA 1310
   1247 TGCCAGCTGCTGAGTGTGATACAGCTGCACTCTTCACTGAGATCA 1306
QY 1311 CAGCTCAGTGCAGTGTGATACAGCTGCACTCTTCACTGAGATCA 1370
   1307 CAGCTCAGTGCAGTGTGATACAGCTGCACTCTTCACTGAGATCA 1366
QY 1371 ATAAACATGTCACAC 1385
   1367 ATAAACATGTCACAC 1381
Db 1367 ATAAACATGTCACAC 1381

RESULT 8
PCT-US95-17111A-49
; Sequence 49, Application PC/TUS9517111A
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Mandis, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and
; TITLE OF INVENTION: Detection of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17111A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/340,426
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; TELEPHONE/DOCKET NUMBER: 0609.3840002
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; PCT-US95-17111A-49

Query Match 74.9%; Score 1080.2; DB 5; Length 1381;
Best Local Similarity 94.4%; Pred. No. 3.5e-292;
Matches 1317; Conservative 0; Mismatches 53; Indels 25; Gaps 18;

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Db	1	TTTTTTTTTGTAGATGAGTGTTCCTCCTTGTGTGGCCAGGCTGAGTGCATATGGCGCAAT	60
Qy	62	CTCAGCTACCGCAACCTCCGCTCCCGGGTTCAAGCAATTCCTGCTCAGCTCCCC	121
Db	61	CTCAGCTACCGCAACCTCCGCTCCCGGGTTCAAGCAATTCCTGCTCAGCTCCCC	120
Qy	122	AGTACGTGGGAAATACAGGCAATGTGACCGCTCGGGCTAATTTTGTATTTTTTTTGT	181
Db	121	AGTACGTGGGAAATACAGGCAATGTGACCGCTCGGGCTAATTTTGTATTTTTTTTGT	179
Qy	182	AGAGATGAGAGTTT--CTCCATGTTGGTCAGGCTGTCTGAACTCCGCACTCAGATGAT	239
Db	180	AGAGATGAGAGTTTAACTCCATGTTGGTCAGGCTGTCTGAACTCCGCACTCAGATGAT	239
Qy	240	CCCTCCGCTCTCGGCTCCCAAAAGTCT--AGATACAGAGCTGGCCACCATCCCGGG--CT	295
Db	240	CTCCCGCTCTCGGCTCCCGCAAAAGTCTCAGATTTACAGGCAATGACCATCCCGGGCT	299
Qy	296	CTGCTGTGCTAATTTTTGTGTAGAAACAGGGTTTTCAGTGATG--TGCCCAAGCTGGTCTC	354
Db	300	CTGCTGTGCTAATTTTTGTGTAGAAACAGGGTTTTCAGTGATGTTGCCAAGCTGGTCTC	359
Qy	335	CTGAGCTCAAGCAGTTCACACTCTGCTCAGCTCTCCAAAGTGTGGGATTTACAGGCTGTGAG	414
Db	360	CTGAGCTCAAGCAGTTCACACTCTCAGCTCTCCAAAGTGTGGGATTTACAGGCT--CAG	418
Qy	415	CGGTGCGTGGGCTTTTTTATTTTTTAAAGACACAGGGTGTCCACCTTTACCCAG	474
Db	419	CGGTGCTGGGCTTTTTTATTTTTTAAAGACACAGGGTGTACCACTTTACCCAG	478
Qy	475	ATGAAGTCAGTGTGTGTATCACAGCTACGACCTCACTCACTCTGAGATCAGC--AT	533
Db	479	ATGAAGTCAGTGTGTGTATCACAGCTACGACCTCACTCACTCTGAGATCAGCAAT	538
Qy	534	CTCTCCGCTCAGCCGCCCAAGTAGTGGGAGCCAAAGACATGACACATACACTCTGGTCA	593
Db	539	CTCTCCGCTCAGCCGCCCAAGTAGTGGGAGCCAAAGACATGACACATACACTCTGG--TA	597
Qy	594	ATTTTATTTTTTATTTTTTAAATTTTTTGAAGACAGAGTCTCAACTCTGTCAACCCAGCTGGA	653
Db	598	ATTTTATTTTTTATTTTTTAAATTTTTTGAAGACAGAGTCTC--ACTCTGTCAACCCAGCTGGA	656
Qy	654	GTGCAATGGGCGCAATCTTGGGTCACACGCAACCTCTGCTCCCGGGTTCAAGTATTTCTCC	713
Db	657	GTGCAATGGGCGCAATCTTGGGTCACACGCAACCTCTGCTCCCGGGTTCAAGTATTTCTCC	716
Qy	714	TGGCCAGGCTCTGTAGTAGCTGGGACTACAGGCGGCCCAACAGGCTAGCTAAATTTTTTT	773
Db	717	TGGCCAGGCTCTGTAGTAGCTGGGACTACAGGCGGCCCAACAGGCTAGCTAAATTTTTTT	776
Qy	774	GTAATTTTACAGATGGGG--TTACACATGTTCCGCAAGTTGATCTTGAATCTGTGAC	832
Db	777	GTAATTTTACAGATGGGGTTTACACATGTTCCGCAAGTTGATCTTGAATCTGTGAC	836
Qy	833	TTTGATATCTCGGCGCTCGGCT--CCCAAGTCTGGGATTTAGAGGCTAGGACACGACG	891
Db	837	TTTGATATCTCGGCGCTCGGCGCTACCCAAAGTGTGGGATTTACAG--GTGTGACTCTAC	894
Qy	892	CCCGGCTAATTTTTTAAATTTTTTGTGTTGAATGAATCTCACTCTGTTTACAGGCTG	951
Db	895	GCGGCGCTAATTTTTTAAATTTTTTGTGTTGAATGAATCTCACTCTGTTTACAGGCTG	954
Qy	952	GAGGCAATGGCCAAATCTGGGCTCACTGCAACCTGCGCCCGGGCTCAAGGATTTCT	1011
Db	955	GAGGCAATGG--CAAAATCTGGGCTACTGCGCAACCTCTGCTCCCGGG--TCAAGGATTTCT	1012
Qy	1012	CTGTCTCAGGCTTCCCAAGCAGCTGGGATTTACGGGCACTGTGCCACCAACCCGCTAAT	1071
Db	1013	CTGTCTCAGGCTTCCCAAGCAGCTGGGATTTACGGG--ACGTGCACCAACCCGCTAAT	1070
Qy	1072	TTTGTATTTTCAATTAGAGCGGGGTTTACCATTTTGTACGGCT--GGTCCAAAGTCT	1130
Db	1071	TTTTGTATTTTCAATTAGAGCGGGG--TTTACCAATTTTGTACGGCTGGGCTCAAACTCT	1128

Qy	1131	GATCAGAGGACCCACACCTCCCTCAGCCTTCCCAAGTGGGAAATACAGGCGTAGGCA	1190
Qy	1131		
Db	1129	GACCTCAGGTGACCCACCTGCTCCTCAGCCTTCCCAAGTGGGAAATACAGGCGTAGGCA	1188
Qy	1191	CCTCACCAGCGGGCTAATTTAGATATAAAAAATATGTACCAATGGGGGCTTGTGTATG	1250
Db	1189	CCTCACCAGCGGGCTAATTTGGAAATATAAAATATGTACCAATGGGGG--TCTGCTATGT	1246
Qy	1251	TGGCCAGGCTGGTCTCAACTCTTGGCTTCATGCAATCCTTCCAATGAGCCACAAACC	1310
Db	1247	TGCCAGGCTGGTCTCAACTCTTGGCTTCAGTCAATCTTCCAATGAGCCACAAACC	1306
Qy	1311	CAGCCAGTCACATTTTTTAAACAGTTCATCTTTATTTAGTATCTAGAAAGTAAATCA	1370
Db	1307	CAGCCAGTCACATTTTTTAAACAGTTCATCTTTATTTAGTATCTAGAAAGTAAATCA	1366
Qy	1371	ATAAAGATGTCAAAC	1385
Db	1367	ATAAAGATGTCAAAC	1381

RESULT 9  
US-08-975-080-35  
; Sequence 35, Application US/08975080

GENERAL INFORMATION:

APPLICANT: Altieri, Dario C.  
TITLE OF INVENTION: SURVIVIN

TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION

NUMBER OF SEQUENCES:	35
----------------------	----

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN, LEWIS &  
STREET. 1800 M Street, N.W.

STREET: 1800 M S  
CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20036-5869

```

; COMPUTER READABLE FORM
; MEDIUM TYPE: FLOPPY

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COMPUTER: IBM PC COMP

OPERATING SYSTEM: PC-DOS

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; SOFTWARE: PatentIn Release #1.0
; CURRENT APPLICATION DATA:

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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,080
;

```

AFFILIATION NUMBER: 00/00/00/00  
 FILING DATE: 20-NOV-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 6  
FILING DATE. 20-NOV-1996

ATTORNEY/AGENT INFORMATION: FILING DATE: 20-NOV-1996

```

; AI TORNEI/AGENT INFORMATION.
;
; NAME: Adler, Reid G.

```

REGISTRATION NUMBER: 30,

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION  
TELEPHONE: 202-467-7000

TELEPHONE: 202-467-7000  
TELEFAX: 202-467-7176

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 14796 base pairs  
TYPE: nucleic acid

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; TYPE: nucleic acid
; STRANDEDNESS: single
;

```

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-975-080-35

Query Match	33.08%
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Query	Local Similarity	Global Similarity
Best Local Similarity	69.8%	69.8%

Matches 877; Conservative

Only 1 nucleotide (GAGATGGAGCTT)

QY L TTTTGGAGATGGAGCT

Db 5380 TTTTCTTGAGATAGAG-TTTCACCTCTTGTGCCCAGGCTGGAGTGCATGGTCAA 543

QY	61	TCCTAGGCTCACCGAAACCTCCGCCCTCCCGGGTTCAAGCAGATTCTCTGCTCAGCCCTCC	120
Db	5439	TCCTGGCTACTGCAACCTCTGCGCTCTCGGGTTCAAGATATCTCTCCTCAGCCTCC	5498
QY	121	CAGTAGCTGGGATTACAGCAGATGTGTACACCCAGCGCTCGGCTAATTTGGATTTTTTTAG	180
Db	5499	AAGTAACTGGGATTACAGGGAAGTCCACACCCAGCTAATTTT---TGTATTTTAA	5555
QY	181	TAGAGATGGAATTTCTCCATGTGGTCAAGCTGTCTGAACTCCCGACCTCAGATGATC	240
Db	5556	TAGAGATGGGGTTTCCACACATTCGCCAGCGTGGCTGTGAATCTGTACCTC---GTGATT	5613
QY	241	CCCTCGCTCGGCCCTCCCAAGTGGTATACAGAGACTGGCCACCATGCCCGCTCTGCC	300
Db	5614	CGCCCACTTGGCTTCCCAAGTCTGT---GATTACAGGGGTGAACCCACACGCTGTGGC	5670
QY	301	TGCGTAAATTTTGTGTAGAAACAGGGTTTCACTGATGTGCCCCAAGCTGGTCTCGT---	357
Db	5671	TTTTTTTTTTTGTGT- GAGACACAGTTTACTCTGTTAACCCAGGCTGGAGTAAAGTG	5729
QY	358	--AGCTAAGCAGTCCACACTGCTCAGCCTCCCAAGTGCAGGGATTACAGCGCTGACG	415
Db	5730	CTGATATCGGATCTACGTCAACCTCCGCTCGGGCTCAAGTATTTGGCTGGTTAGC	5789
QY	416	CGTGCCTGGCCCTTTTATTTATTTTATTTTAAAGACAGAGTGTCCACTCTTACCCAGGA	475
Db	5790	CTCCCAAGTACCGCAGATATACAGGACATGTCCACACCCACCCAGTAAATTTTGTATTTT	5849
QY	476	TGAAGTGCAGTGTGTGATCA--CAGCTCAGCTCAGCCTTCACTCTCGATGATG--CA	532
Db	5850	GGTAGAGACAGAGTTTCCATGTGTGGCCAGGCTGGTTTGAAGTCTGTGACTCTGACTAGTGA	5909
QY	533	TCCTCTGCTCAGACTCCCAAGTAGCTGGGACCAAGACATGCACCATACACTGTC-	591
Db	5910	TCACCCGCTCAGCCCTCCCAAGTGTGATTAATAGTGTGAGCCACACACTGTGCC	5969
QY	592	-----TAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	640
Db	5970	TCAGAGATATTTTATTTTATTTTAAATTTTATTTTATTTTATTTTATTTTATTTTATTTT	6028
QY	641	CACCCAGGCTGAGTGCAGTGGCGCAATCTGGCTCACTCAACCTGTGCTCCCGGGTT	700
Db	6029	CGCGTACGGCTAGAGTGCAGGAGGAGATCTCGGCTACTCTCAAGTCTGCCCTCCCAAGTT	6088
QY	701	CAGATTATCTCTGCCCCAGCCTCTGAGTAGCTGGGACTACAGGCGC---CCACGACG	757
Db	6089	CAGGCATTCTCTGCTCAGCCTCCCGAGTACTGGGACTACAGGGGCCGCGCACACACA	6148
QY	758	CTAGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	816
Db	6149	CCCGGTAATTTTGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	6208
QY	817	TCCTGATCTGTGACCTTGTGATCTGCTGCGCTCGGCTCCCAATGTGCGGGATTACAG	876
Db	6209	TCCTGATCTGTGACCTTGTGATCTGCTGCGCTCGGCTCCCAATGTGCGGGATTACAG	8268
QY	877	GGTAGGCACACAGCGCGGCTTATTTTAAATTTTGTGTTGAATGAAATCTCACT	936
Db	6269	GGTAGGCACACACCGGCT-----AATTTTATTTTATTTTATTTTATTTTATTTTATTTT	6320
QY	937	CTGTTACCCAGGCTGGAGTGAATGGCCAAATCTGGGCTACATCGCAACCTGTGCTCCG	996
Db	6321	CTGTCACCTGGGCTCGAAGTGAAGTGG--TACACCATTAAGTCACTGCGAGCTTCAATCTCG	6379
QY	997	GGCTAAGGAGATTCCTGTCTACACCTCCCAAGCAGCTGGGATTACGGGACCTGCCAC	1056
Db	6380	AGCTCAAGTGAATCTCCACCACTCATCTCACAAGTAATTTGGGACATACAGTGCACCCAC	6439
QY	1057	CACACCCGGTAATTTTGTAT-----TTTCAATGAGGCGGGGTTTCAAC	1101
Db	6440	CATGCGCACTAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT	6499
QY	1102	CATATTTTCAGGGCTGATCAAACTCCGAGCCTGAGGAGACCCACCTCCCTCAGCCTTC	1161

[illegible]

Db	5850	GGTAGAGCAGAGTTTCACCATGTTGGCCAGGCTGGTTTTGAACTCGAGCCTCAGGTGA	5909
Qy	533	TCCTCTCCCTCCAGCTCCCAAGTAGCTGGGACCAAGACATGACACACTACCTGGC-	591
Db	5910	TCACCCGGCTCAGCGCTCCCAAGTACTAGATTATAGTGTGAGCACACACACTGGCC	5965
Qy	592	-----TATTTTTTTTTTTTTTTTTTTTTTTTTTTTGTGAGCAGAGTCAACTCTGT	640
Db	5970	TCAGGAAGTATTTTTTATTTTTTAAATTTATTTTATTTTATTTGAGATGAGCT-TGCTGT	6028
Qy	641	CACCCAGGCTGAGTGCAGTGGCGCAATTTGGCTCATTGCACATCACTCTGCTCCGGTT	700
Db	6029	CGCCAGGCTAGATGCAGGACGGAGATCGGCTCACTGCAAGCTCCGCCCAAGTT	6086
Qy	701	CAATTTATTCCTCGGCCCGAGGCTCGAGGTACTGGGACTACAGGCG-CCACACAG	757
Db	6089	CACCCATTCCTCGCTCAGCCTCCCGAGTACTGGGACTACAGGCGGCCGCGCACANA	6144
Qy	758	CGTAGCTAATTTTTTTTATTTTATTTAGTAGAGATGG-GTTACACATGTTCCGCAAGTTGA	816
Db	6149	CCCGCTAATTTTTTTTATTTTATTTTATTTAGTAGAGAGCGGTTTTCACCGTTAGGACAGAGG	6208
Qy	817	TCCTGATCTCTGAGCCTTGATCTGCTGCTCCGCGCTCCCAACTGCTGGGATTACAG	876
Db	6209	TCCTGATCTCTGAGCTCGATCTGCTGCTGCTCGGCTCCCAAGTCTGGGATTACAG	6266
Qy	877	GCCTGAGGCACACAGCCCGGCTTATTTTTTAATTTTGTTTTGTAATGGAATCTCACT	936
Db	6269	GTGTAGGCACACACCCGGCT-----ATTTTTTTTTTTTGGACAGGACTCACT	6322
Qy	937	CTGTATACCCAGGCTGGAGTGAATGGCAATCGCGCTCACTGCAACCTCTGCTCCCG	996
Db	6321	CTGTACTCTGGCTGGAGTGCAGTGG-TACACCAATAGCTACTGTCAGACCTCGAATCTCG	637
Qy	997	GGCTCAAGCGATTCTCTGTCAGCCTCCCAAGCAGCTGGGATTACAGGCACTCTGCAC	105
Db	6380	AGCTCAAGTGTCTCCACACTCTCACTCCACAAAGTAATTTGGAGTCAAGGTGCACCCAC	643
Qy	1057	CACACCCCGGTAATTTTTGTAT-----TTTCATTAGAGGGGGGTTTCAC	110
Db	6440	CATGCCCACTAATTTATTTATTTATTTATTTATTTATTTTTCATAGAGATGAGAGTTCC	649
Qy	1102	CATATTTGTCAAGCTGTCTCAACCTCTGACTCAGAGTGAACCACTGCTCAGCCTTC	116
Db	6500	TGTGTTTTCACAGGCTGTCTTGAACCTCTGTGACTCAGGGGATCTTTTGGCTGGGCTCC	655
Qy	1162	CAAACTGCTGGATTACAGGGGTGGGCCACTCAACGAGCGGGTAAATTAGATAA	1218
Db	6560	CAAGGCTGAGATTTACAGGCACTGAGCCACCGTCCCACTAGGAATCATTTTAA	6616

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US-09-496-694B-3
; Sequence 3, Application US/09496694B
; Patent No. 633194
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Coscert
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPI-0439
; CURRENT APPLICATION NUMBER: US/09/496,694B
; CURRENT FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1998-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 3
; LENGTH: 14796
; TYPE: DNA
; ORGANISM: Homo sapiens

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?   FEATURE:
?   NAME/KEY: CDS
?   LOCATION: (2811)...(2921)
?   NAME/KEY: CDS
?   LOCATION: (31/4)...(3283)
?   NAME/KEY: CDS
?   LOCATION: (5158)...(5275)
?   NAME/KEY: CDS
?   LOCATION: (11955)...(12044)
US-09-436-634B-3

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Query Match	33.0%;	Score 475.4;	DB 4;	Length 14796;
Best Local Similarity	69.8%;	Pred. No. 7.8e-123;		
Matches 877;	Conservative	0;	Mismatches 321;	Indels 59;
				Gaps 15;

QY	1	TTTTTTTTTTAGATGGAGTTTGGCTTGTGTGGCCAGGCTGGAGTGCATGGCCAA	00
Db	5380	TTTTTTTTCTGAGATAGAG-TTTCACCTCTGTGGCCAGGCTGGAGTGCATGGCCAA	5438
QY	61	TCGCACCTACCCGAAACCTCGCGCTCCGGGGTCAAGAGATTTCCTCGCCACACCTCC	140
Db	5439	TCCTTGGCTACAGCAACCTCTGCTCTCGGGTTCAAGATATCTCTCGCTCAGCCTCC	5498
QY	121	CAGTAGCTGGGATATACAGGCATGTGCACCCACGCTCGGCTAATTTTGTATTTTTTAC	180
Db	5499	AAGTAATCGGATATACAGGGAAGTGCACACCCACCACTAATTTT--TGATATTAC	5555
QY	181	TAGAGATGACGTTTCTCCATGTTTGGTCAGGCTGGCTGGAACTCCGACCTCAATATC	240
Db	5556	TAGAGATGGGGTTTACACCACTTGGCCAGGCTGGCTTGAATCTGTACCTC--GTATTT	5613
QY	241	CTCCGCTCGGGCTCCCAAGAGTGTAGATATACAGACTGGCCACCATGCGGGCTGCG	300
Db	5614	CGGCCACTTGGGCTCCCAAGAGTGTG--GATTACAGGGGTGAACCAACCACTGGC	5670
QY	301	TGGCTAATTTTGTGTAGAACAGGGTTTCACTGATGTGCCAAGCTGGTCTCTG--	357
Db	5671	TTTTTTTTTTTTGTCT-GAGACACAGTTTCACTGTTACCCAGGCTGGAGTAGGTTG	5729
QY	358	--ACCTAACACAGTCAACCTGCGCTCAAGCTCCCAAGTGGCTGGATATACAGCGTCA	415
Db	5730	CTGTATCTGGATATCACTGCAACCTCGGCTCCGGGCTCAATGATTTGCTGTTCA	5789
QY	416	CGTGGCTGGCTTTTATTTTATTTTTTTTAAAGACACAGTGTCCCACTTAACCAAGA	475
Db	5790	CTCCCAAGTAGCCGAGATTACAGGCATGTGCCACACACCAAGTAATTTTGTATTTT	5849
QY	476	TGAGATGAGGATGATATCA--CAGTCACTGACACCTTCACTCGAGATCAAG-CA	532
Db	5850	GGTGAGACAGAGTTTACCATGTGTGGCCAGCGTGGTTTGAATCTCGACTCAGHGA	5909
QY	533	TCCTCTGGCTCAGCGTCCCAAGTAGTACTGGGACCAAGACATGACACACTACACTGGC	591
Db	5910	TCCACCGGCTCAGCGTCCCAAGTGTGTGATATAGGTGAGACACACACTGGCC	5968
QY	592	-----TATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	640
Db	5970	TCAGAGATATTTTATTTTATTTTAAATTTATTTATTTATTTTATTTGAGATGAGCT	6028
QY	641	CACCCAGGCTGAGTGCAGTGGCCAACTTGGCTCACTGCAACTCTGCTCCCGGTT	700
Db	6029	CGGCCAGGCTGAGTGCAGGAGCGGATCTCGGCTCACTGCAAGCTCCGCCCAAGTT	6088
QY	701	CAGTATTTCTCGCCCCACACCTCCAGTACTGGGATACAGGCG--CCACCAAG	757
Db	6089	CAGGCAATTTCTCGCTCACTCAGCTCCGAGTAGTGGGATACAGGCGCCGCCACACAA	6144
QY	758	CTACACTAATTTTGTATTTTGTATTTAGTAGAGATGG-CTTCACCACTGTTGCCAGGTGA	816
Db	6149	CCGGCTAATTTTGTATTTTGTATTTTGTATTTAGTAGAGAGGGGTTTACCGTGTACAGAGGG	6208
QY	817	TCTGATCTGACCTTGATCTGCTCTGCTCGGCTCCCAAACTGCGGGATATACG	876

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Db 6209 TCTTGATCTCTGACCTGCTGATTCGCTGCGGCTCCCAAGATGCTGGATTACAG 6268
QY 877 GCGTAGCCACACGCGCGGCTTATTTTAAATTTGTTTGAATGATCTACT 936
Db 6269 GTGTAGGACACACCGGCT-----ATTATTTATTTTATGAGAGGACTACT 6320
QY 937 CTGTACCCAGGCTGAGATGCAATGGCCAAATCTGCGTCACTGACCTGCTGCGCG 996
Db 6321 CTGTACCTGGGCTGCTGAGTGG--TACACATAGCTCACTGAGCTGCACTCTCG 6379
QY 997 GCGTCAACGATCTCTGCTGCTGACCTCCAGACGCTGGGATTACGGGACCTGCCAC 1056
Db 6380 AGCTCAAGTATTCCTCCACCTCATCTACAAATGGAGTACAGTACAGTACCCAC 6439
QY 1057 CACACCCGCTAATTTTGTAT-----TTTCATTAGAGCGGGTTTAC 1101
Db 6440 CATGCCACCTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 6499
QY 1102 CATATTTGTCAGGCTGCTGCTCAACCTCTGACCTGAGTGACCCAGCTGCACTTC 1161
Db 6500 TGTGTTGTCAGGCTGCTGCTGAGCTGAGCTGAGGAGTTCCTTTCCTGGGCTCC 6559
QY 1162 CAAGTGTGGATTACAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 1218
Db 6560 CAAGTGTGATTTACAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 6616

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RESULT 12
US-09-813-817-3/c
; Sequence 3, Application US/09813817
; Patent No. 6340583
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001178
; CURRENT APPLICATION NUMBER: US/09/813,817
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; LENGTH: 59065
; SEQ ID NO 3
; TYPE: DNA
; ORGANISM: Human
US-09-813-817-3

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Query Match 28.9%; Score 416.4; DB 4; Length 59065;
Best Local Similarity 67.7%; Pred. No. 4,3e-106;
Matches 815; Conservative 0; Mismatches 326; Indels 63; Gaps 14;

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QY 42 CTGAGATGCAATGGGCAATCTGAGTCAACGCACTCGGCTCCGGGTTCAAGCAT 101
Db 15163 CTGAGAGGAGTGGCGCATCTGACGACACTGCACTCCATCTCCAGGTTCAAGCAT 15104
QY 102 TCTCCGCTCAAGCTCCGCAATGCTGGGATTACAGGATGCAAGCCAGCTGCGCTA 161
Db 15103 TCTCCGCTCAAGCTCCGCAATGCTGGGATTACAGGATGCAAGCTGCGCTA 15044
QY 162 ATTTGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 221
Db 15043 ATTTT---TGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 14987
QY 222 CTCCGAGCTCAAGATGCTCCCTGCTGCTGCGCTCCCAAGTCT--AGATACAGAGTGG 280
Db 14986 CTCTGAGCTCAAGTGGTATCGGCTGCTGAGCTCCCAAGTGGTGGATTACAGGCTGG 14927
QY 281 CCACCATGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 340
Db 14926 AGCCACCGGCGCCACCTCATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 14867
QY 341 CCCAAGCTG-----GTCTCCTGAGACTCA 363

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Db 14866 CCCAGGCTGAGTGCAGTGGCGGATCTGACTCACTGCAAGCTCGGCTCCGGGTTCA 14807
QY 364 AGCAGTCAACCTGCTGAGCTGCTGAGGATTACAG--GCGTAGCCGCTGCC 421
Db 14806 GCGCATATTCCTGCTGAGCTGAGTGGGATGAGGAGGAGTACAGAGTGGCTCCACCATGCC 14747
QY 422 TGGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 481
Db 14746 TGGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 14687
QY 482 GCAGTGTGTATGATCAGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 541
Db 14686 -GCATCTCTGAGTCTGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 14628
QY 542 CTCAGCTCCCAAGTGTGGGAGCCAAAG-----CATGACACACTACAGCTGCTAAT 596
Db 14627 GTGAGCCACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 14568
QY 597 TTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 656
Db 14567 TATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 14509
QY 657 CAGTGGCGCAATCTTGGCTCACTGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 716
Db 14508 CAGTGCATGATGTTGGGCGCACTGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 14449
QY 717 CCCAGCTCC--TGAGTGTGGGACTACAGGCGC--CGACCAAGCTAGCTAATTTT 770
Db 14448 CTCAGCTCCCAAGTGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGT 14391
QY 771 TTTGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 829
Db 14390 TTTGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 14331
QY 830 ACCT--TGATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 887
Db 14330 ACCTCAAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 14271
QY 888 CAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 946
Db 14270 CAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 14211
QY 947 GCGTGGAGTGCATGCGCAATGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1006
Db 14210 GCGTGGAGTGCATGCGCAATGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 14151
QY 1007 ATTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1066
Db 14150 ATTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 14091
QY 1067 TAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1125
Db 14090 TAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 14031
QY 1126 CTCTGAGCTCAAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 1185
Db 14030 CTCTGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 13971
QY 1186 AGCC 1189
Db 13970 AGCC 13967

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RESULT 13
US-09-978-197-3/c
; Sequence 3, Application US/09978197
; Patent No. 6403353
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001178DIV

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Db 37001 CCAGAAACTTTTAAATATGTTTGAACACACTTGGGCACTGTCAATCTATTTCCCACTG 36942
QY 361 TCAAGCAGTCCACCTGCTCAGCCCTCCAAAGTGTGGATTACAGGCGTGCAGCCGTC 420
Db 36941 TTAATACACACAGATTTTG-----AAGACATAGATGATAAACAAGACAGATGTT 36892
QY 421 CTGGCCCTTTTATTTATTTTATTTTAAAGACAGAGTGTCCCACTCTTCCCAAGATGAAG 480
Db 36891 TCATTGAGTTTGTCTCTTTTAAAGACACA-GGCTCTTGTCTGTCACTCCAGCTGGAG 36833
QY 481 TGCAGTGTGTGATCAGACTCACTGACGCTTCAACTCTGAGATCAAG-CATCTCTCT 539
Db 36832 TGCAGTGTGCAACATCAGCTAGCTAGACTTGAATCTGCTGCTCAAGCGCTTCC 36773
QY 540 GCGTCAGCTCCCAAGAGTGGGACCAAAAGACATGACCACTACCTGCG-----591
Db 36772 ATCTGGCCCTCCCAAGATGGGGATTAAGGACATGAGCCACTCCCTGCGCTTAATAA 36713
QY 592 -----591
Db 36712 TTTTATGTTGACTACATGTTGAATAAGTGCATATGTTGGATTAACATATATATAT 36653
QY 592 TAAATTTTATTTTATTTTATTTTATTTTGAAGAGAGTCTC-----AACTGTGTACC 644
Db 36652 ATATATATATATTTTATTTTATTTTATTTTGAAGACAGTCTCTGCTGTGTGACCC 36593
QY 645 CAGGCTGAGTGCAGTGGGCAATCTTGCTCACTGCACTGCTGCTCCCGGGTTCCAG 704
Db 36592 CAGGCTGAGTGCAGTGGGCAATCTTGCTCACTGCACTGCTGCTCCCGGGTTCCAG 36533
QY 705 TTAATCTCTGCGCCCAAGCTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 761
Db 36532 CCAATCTCTCACTGCACTGCGCCCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 36473
QY 762 GCTAA--TTTTTGTATTTTGTATGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 818
Db 36472 GCTAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 36413
QY 819 TTAGTCTCTGAGCTGTGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 878
Db 36412 TCGATCTCTGAGCTGTGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 36353
QY 879 GTGAGCCACGACGCGCGCTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 938
Db 36352 GTGAGCCACGACGCGCGCTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 36298
QY 939 GTTACCCAGGCTGAGTGTGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 998
Db 36297 GTTATTCAGGCTGAGTGTGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 36238
QY 999 CTCAGGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1058
Db 36237 CTCAGGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 36178
QY 1059 CAGCCGCTTATTTTGT--ATTTTCAATTTAGGCGGGGTTTCACTATTTTGTGAGCG 1115
Db 36177 TCCCGGCTTATTTTGT--ATTTTCAATTTAGGCGGGGTTTCACTATTTTGTGAGCG 36118
QY 1116 TGGTCTCAAACTCTGAGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1175
Db 36117 TGGTCTCAAACTCTGAGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1175
QY 1176 TACAGGCGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 1222
Db 36059 TACAGGCGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 36013
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RESULT 15
US-08-687-080-101/c
; Sequence 101, Application US/08687080
; Patent No. 5965427
; GENERAL INFORMATION:
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APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSER: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,080
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,126
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
FAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 5543 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: 3' END OF INTRON 19 OF RAD50 GENOMIC
US-08-687-080-101
Query Match 27.8%; Score 400.8; DB 2; Length 5543;
Best local similarity 72.1%; Pred. No. 3.5e-102;
Matches 610; Conservative 0; Mismatches 217; Indels 19; Gaps 6;
QY 592 TAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 651
Db 1274 TGACTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1216
QY 652 GAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 711
Db 1215 GAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1156
QY 712 CTGCCCCAGCTCTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 768
Db 1155 CTGCCCCAGCTCTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1096
QY 769 TTTTGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 827
Db 1095 TTTTGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1036
QY 828 GGAATCTGTGATCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 887
Db 1035 TGACCTGTGATCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 976
QY 888 CAGCCGCGCTTAT--TTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 937
Db 975 CAGCCGCGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 916
QY 938 -TGTACCAAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 996
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Db 915 TTGTACCCAGGCTGAAGTGCATGTGTGATCTGGCTCACTGCATCTGCTCCCA 856
QY 997 GGCTCAAGCATTTCTCTCTCTCAAGCTTCCCAAGCATGTGGATTAAGGGCACTGCCAC 1056
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 855 GGTTCAAGGATTTCTCTGCTCTCAGCTCTGATACCTGGGATTAACAGCGCGTGTAC 796
QY 1057 CACACCCCGCTAATTTTGTATTTTCAATTAGAGGGGGTTTCCACATATTTGTACGGCT 1116
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 795 CACACCTGGCTAATTTTCTATTTTCAAGATGGGGTTTACCATATTTGGCCAGGCT 736
QY 1117 GGCTCAAACTGCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 1176
    ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 735 AGTCTTGAACTCTCTGACCTGACCTGATCCGCTTGCTGGCTCCCAAGTGTGGGAT 676
QY 1177 ACAGGGGTGAGCCACCTCACCAGCCGCTAATTAGATAAAAAATATGTAGCAATGG 1236
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 675 ACAGGATGAGTCACTGCGCTGCGCTCTCTCTTATTTGACTAGTAAATCTCAGCA 616
QY 1237 GGGCTTGTGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1296
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 615 AGCATATCAGACTTTCATGATATCTTTTATACCTTCT--CTCTGCTTTCATTTACT 559
QY 1297 TGAGCCCAACAGCCAGCAGTCAATTTTAAACAGTTACATCTTTATTTAGTATAC 1356
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 558 CTGGCCCTTATTTCTACACTGCTGCTTTTCCCATTAATTTGAATACATTTATCTTGC 499
QY 1357 TAGAAGTATATACATTAACATGTCAAACCTGCAATTCAGTGTACAGAGTCTTTTA 1416
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Db 498 TCTATGTATATTAAGTAAGTAATAATTCTGGAACAAGAGGTACAAAGTAACATAA 439
QY 1417 TAACTT 1422
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Db 438 TACCAT 433

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Search completed: February 1, 2003, 22:42:06  
 Job time : 228 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 20:03:23 ; Search time 330 Seconds  
(without alignments)  
9840.550 Million cell updates/sec

Title: US-09-964-678A-1  
Perfect score: 1442  
Sequence: 1 ttttttttttgcagatgcagag.....ttaacaacagcttagagca 1442

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :  
1: N.Geneseq\_101002:\*  
2: /SIDS2/gcgcdata/geneseq/geneseqn-emb1/NA1980.DAT:\*  
3: /SIDS2/gcgcdata/geneseq/geneseqn-emb1/NA1981.DAT:\*  
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7: /SIDS2/gcgcdata/geneseq/geneseqn-emb1/NA1985.DAT:\*  
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11: /SIDS2/gcgcdata/geneseq/geneseqn-emb1/NA1989.DAT:\*  
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21: /SIDS2/gcgcdata/geneseq/geneseqn-emb1/NA1999.DAT:\*  
22: /SIDS2/gcgcdata/geneseq/geneseqn-emb1/NA2000.DAT:\*  
23: /SIDS2/gcgcdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*  
24: /SIDS2/gcgcdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*  
25: /SIDS2/gcgcdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1442	100.0	1442	24	ABN89470
2	1223.4	84.8	1418	17	AAT27738
3	1078.6	74.8	1381	17	AAQ77883
4	1077	74.7	1381	17	AAT27765
5	587.8	40.8	65608	24	ABL62910
6	587.8	40.8	65608	24	ABL64414
7	587.8	40.8	65608	24	ABL67668
8	524.4	36.4	62944	24	ABL66947
9	524.4	36.4	62944	24	ABL68262

C	10	517.2	35.9	33747	22	AAK69279	Human immune/haema
C	11	517.2	35.9	33747	22	AAK73093	Human immune/haema
C	12	513.4	35.6	43545	24	ABK85018	Human cadherin-11k
C	13	513	35.6	21470	23	ABK42270	Genomic sequence #
C	14	511.6	35.5	5262	22	AAK71768	Human immune/haema
C	15	511.6	35.5	5262	22	AAK71769	Human immune/haema
C	16	490.4	34.0	98014	22	ABN96931	Gene #3429 used to
C	17	489.6	34.0	24167	22	ABN96931	Human nervous syst
C	18	479.6	33.3	44820	22	ABN96931	Reference sequence
C	19	479.2	33.2	51719	24	AAK71768	52kb gene fragment
C	20	479.2	33.2	92139	24	AAK71768	92kb gene fragment
C	21	478.2	33.2	31853	22	AAI98993	Human excretory re
C	22	478.2	33.2	31853	22	AAI98993	Human kidney relat
C	23	477.4	33.1	11319	22	AAI63343	Genomic sequence #
C	24	477.4	33.1	11319	22	AAK39682	Human digestive sy
C	25	475.4	33.0	14796	19	AAK90025	Survivin gene. Ho
C	26	475.4	33.0	14796	22	AAK27941	DNA encoding human
C	27	475.4	33.0	14796	22	AAK27941	Human Her-3 genom
C	28	475.4	33.0	14796	22	AAH47531	Gene #3422 used to
C	29	475.4	33.0	14796	22	ABN96924	Lung cancer relate
C	30	475.4	33.0	14796	24	ABN96924	Lung cancer relate
C	31	475.4	33.0	14796	24	ABN96924	Kidney cancer rela
C	32	475.4	33.0	14796	24	ABN96924	Human transporter
C	33	471.2	32.7	12542	22	AAI72317	Human genomic DNA
C	34	467	32.4	15041	22	AAI72317	Human cardiovascular
C	35	466.8	32.4	9236	22	AAK535921	Rhesus gene locus:
C	36	466.8	32.4	9236	22	AAK535921	Rhesus gene locus:
C	37	466.8	32.4	9236	22	AAK535921	Rhesus gene locus:
C	38	461.8	32.0	12026	22	AAK67211	Human immune/haema
C	39	461.8	32.0	36221	22	AAK67211	Human immune/haema
C	40	459.4	32.0	2368	22	AAK69566	Human death-associ
C	41	459.4	31.9	30110	22	AAK89230	Human immune/haema
C	42	457.8	31.7	160552	22	AAK89230	Human digestive sy
C	43	457.8	31.7	160552	22	AAK89230	Human glycosyl sul
C	44	457.4	31.7	38771	22	ABK84756	Human cDNA diffe
C	45	456.4	31.7	16310	22	AAK81036	Human immune/haema
C	46	456.4	31.7	16310	21	AAK21086	Human low adenosis

## ALIGNMENTS

RESULT 1	ABN89470	standard; DNA; 1442 BP.
ID	ABN89470	
AC	ABN89470;	
XX		
XX		
DT	02-SEP-2002	(first entry)
XX		
DE	Neural thread protein (NTP) encoding nucleotide sequence.	
XX		
XX	Neural thread protein: NTP; Har11 peptide; Alzheimer's disease;	
KW	Dow's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma;	
KW	hypoxia; ischaemia; cerebral infarction; gene; ds.	
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	15..1142
FT		/tag= a
FT		/product= "Neural thread protein"
XX		
PN	W0200234915-A2.	
XX		
PD	02-MAY-2002.	
XX		
PF	25-OCT-2001; 2001WO-US42813.	
XX		
PR	27-OCT-2000; 2000US-0697590.	
XX		
PA	(NIMO-) NIMOX PHARM CORP.	
XX		
PI	Fitzpatrick J, Averback P, Focht MSS, Bibiano R;	

...GACCAATGACCACTGCTAATTTTA 600

QY	601	TTTTATATTTAAATTTTAAATTTTAAAGACAGAGTCTCAACTCTGTCAACCCAGGCTGGAGTGCAGT	660
Db	601	TTTTATATTTTAAATTTTAAATTTTAAAGACAGAGTCTCAACTCTGTCAACCCAGGCTGGAGTGCAGT	660
QY	661	GGCGCAATCTTGGCTCACTGCAACCTCTGCTCCGGGGTTCAAGTATTTCTTCGGCCCA	720
Db	661	GGCGCAATCTTGGCTCACTGCAACCTCTGCTCCGGGGTTCAAGTATTTCTTCGGCCCA	720
QY	721	GCCGCGAGTACTCTGGGACTACAGGCGCCACACAGCCCTAGCTAAATTTTGTATTTT	780
Db	721	GCCGCGAGTACTCTGGGACTACAGGCGCCACACAGCCCTAGCTAAATTTTGTATTTT	780
QY	781	TAGTAGAGATGGGGTTCCACCATGTTCCGAGGTATGTATCTGATCTGAGCACTTGTATC	840
Db	781	TAGTAGAGATGGGGTTCCACCATGTTCCGAGGTATGTATCTGATCTGAGCACTTGTATC	840
QY	841	TGCGTGCCTCGGCTCCCAAGTCTGGGATTTACAGCGGTAGGACACACAGCCGGCTTA	900
Db	841	TGCGTGCCTCGGCTCCCAAGTCTGGGATTTACAGCGGTAGGACACACAGCCGGCTTA	900
QY	901	TTTTATATTTTGTGTTGTTGAAATGGAAATCTCACTCTGTATCCAGGCTGAGTGCAT	960
Db	901	TTTTATATTTTGTGTTGTTGAAATGGAAATCTCACTCTGTATCCAGGCTGAGTGCAT	960
QY	961	GGCGCAATCTCGGCTCACTGCAACCTGCGCTCCGGGCTCAAGCAATTTCTGTGCTCA	1020
Db	961	GGCGCAATCTCGGCTCACTGCAACCTGCGCTCCGGGCTCAAGCAATTTCTGTGCTCA	1020
QY	1021	GGCTCCCAAGCAGCTGGGATTTACGGGCACTGCCACACACCCCGCTAAATTTTGTATTT	1080
Db	1021	GGCTCCCAAGCAGCTGGGATTTACGGGCACTGCCACACACCCCGCTAAATTTTGTATTT	1080
QY	1081	TGATTTAGAGGGGGGTTTCACCATATTTTGTACAGGCTGGTCTCAAACTCCTGACCTCAGGT	1140
Db	1081	TGATTTAGAGGGGGGTTTCACCATATTTTGTACAGGCTGGTCTCAAACTCCTGACCTCAGGT	1140
QY	1141	GACCCACCTGCCTCAGCCCTCCAAAGTGGGATTTACAGGGGTGAGCCACTCACCCAG	1200
Db	1141	GACCCACCTGCCTCAGCCCTCCAAAGTGGGATTTACAGGGGTGAGCCACTCACCCAG	1200
QY	1201	CCGGCTAAATTTAGATTAATAAATATGTAGCAATGGGGGCTCTTGCTATGTTGCCAGGCT	1260
Db	1201	CCGGCTAAATTTAGATTAATAAATATGTAGCAATGGGGGCTCTTGCTATGTTGCCAGGCT	1260
QY	1261	GATTCGCAACCTCTGGGCTGTATGCATCTCTGCAATGAGCCACAACCCAGGCAGTCA	1320
Db	1261	GATTCGCAACCTCTGGGCTGTATGCATCTCTGCAATGAGCCACAACCCAGGCAGTCA	1320
QY	1321	CATTTTAAACAGGTATACATCTTATTTTATTTAGTACTAGAAAGTAAATTCANTAAACATGT	1380
Db	1321	CATTTTAAACAGGTATACATCTTATTTTATTTAGTACTAGAAAGTAAATTCANTAAACATGT	1380
QY	1381	CAAACTCGCAAAATTCAGTGTAGTAAACAGAGTCTTTATTAACCTTTTAAACAAAGCTTTAGAG	1440
Db	1381	CAAACTCGCAAAATTCAGTGTAGTAAACAGAGTCTTTATTAACCTTTTAAACAAAGCTTTAGAG	1440
QY	1441	CA 1442	
Db	1441	CA 1442	
RESULT 2			
AAAT27738			
ID AAAT27738 standard; DNA; 1418 BP.			
XX AAAT27738;			
XX			
DT 13-NOV-1996 (first entry)			
XX			
DE Neural thread protein coding sequence.			
XX			
NW Neural thread protein; NRP; diagnosis: detection:			





AA077883	ID	AA077883	standard; cDNA; 1381 BP.
XX	AC	AA077883;	
XX	DT	06-JUL-1995	(first entry)
XX	DE	Neural thread protein AD10-7 cDNA.	
XX	KW	Neural thread protein AD10-7; Alzheimer's;	neuroectodermal tumours;
XX	XX	malignant astrocytomas; glioblastomas; ss.	
XX	OS	Rattus rattus.	
XX	PN	M09423756-A.	
XX	PD	27-OCT-1994.	
XX	PF	20-APR-1994;	94WO-US04321.
XX	PR	20-APR-1993;	93US-0050559.
XX	PA	(GENO ) GEN HOSPITAL CORP.	
XX	PI	De LA MONTE SM, Wands JR;	
XX	DR	WPI; 1994-341497/42.	
XX	XX	Detection of neural thread proteins - to detect sporadic and	
XX	PT	familial Alzheimer's disease, neuroectodermal tumours, malignant	
XX	PT	astrocytomas and glioblastomas (Enq).	
PS	XX	Example 4; Fig 16R; 158bp; English.	
CC	CC	AA077883 is the AD10-7 neural thread protein (NTP) cDNA. This	
CC	CC	sequence was used in the development of an antibody dependent	
CC	CC	method, for the detection of NTPs. This new method could be	
CC	CC	used to diagnose Alzheimer's disease (differentiating between	
CC	CC	sporadic and familial), neuroectodermal tumours, malignant	
CC	CC	astrocytomas and glioblastomas.	
SO	Sequence	1381 BP; 296 A; 385 C; 301 G; 399 T; 0 other;	
Query Match	74.8%;	Score 1078.6; DB:15; Length 1381;	
Best Local Similarity	94.3%;	Pred No. 1.4e-277;	
Matches 1316;	Conservative	0; Mismatches 54; Indels 25; Gaps	18;
0Y	2	TTTTTTTGGAGATGAGTGTTCGCTCTGTGTTGCCAGGCTGGAGTGCATGGGCAAT	61
Db	1	TTTTTTTGGAGATGAGTGTTCGCTCTGTGTTGCCAGGCTGGAGTGCATGGGCAAT	60
0Y	62	CTCAGCTCACCGCAACCTCCGCTCCCGGGTTCAGGCAATTCCTGCTCAGCTCCCC	121
Db	61	CTCAGCTCACCGCAACCTCCGCTCCCGGGTTCAGGCAATTCCTGCTCAGCTCCCC	120
0Y	122	AGAGAGTGGAGTTAAGCGCATGTGCACCCAGCGCTGGCTAATTTTGTATTTTGTAGT	181
Db	121	AGAGAGTGGAGTTAAGCGCATGTGCACCCAGCGCTGGCTAATTTTGTATTTTGTAGT	179
0Y	182	AGAGATGAGATT--CTCATGTGTGTGTCAGGCTGTCGAACTCCGAGCTCAGATGAT	239
Db	180	AGAGATGAGATTAACTCATGTTGTGTAGCTGTCTCGAATCCGACCTCAGATGAT	239
0Y	240	CCCTCGCTCTGCGCTCCCAAGTCT--AGATACAGAGCATGGCCACCATGCCCCCT	299
Db	240	CTCCCGCTCTGCGCTCCCAAGTCTGAGATACAGAGCATGAGCCACCATGCCCCCT	299
0Y	296	CTGCTGCTAATTTTGTGTAGAAACAGGCTTCACTGATG-TGCCAAGCTGTCTC	354
Db	300	CTGCTGCTAATTTTGTGTAGAAACAGGCTTCACTGATGTTGCCAAGCTGTCTC	359
0Y	355	CTGAGCTTACAGCACTGCTCCTCAGCTCCCAAGTCTGGAGTTAAGGCTGGGAG	414

Db	360	TCACGCTAACACAGCTCCACCTGCCTCAGCCTCCCAAGATCTGGGATTACAGGCGT - CAG 418
OY	415	CCGTCGCTGGCCTTTTATTTATTTATTTTAAAGACACAGGTGGCCACGCTTACCAG 474
Db	419	CCGTCGCTGGCCTTTTATTTATTTTAAAGACACAGGTGTACACCTTTACCCAG 478
OY	475	ATGAAGTGCAGTGGTGTGATCACAGGTCATGCACGCTTCAACTCTGATCAATC - AT 533
Db	479	ATGAAGTGCAGTGGTGTGATCACAGGTCATGCACGCTTCAACTCTGATCAATC 538
OY	534	CTCTCTGCTCACCCTTCCCAAGTAGCTGGGACCAGATGCACATGCACATCCTGGCTA 593
Db	539	CTCTCTGCTCACCCTTCCCAAGTAGCTGGGACCAGATGCACATGCACATCCTGGCTA 597
OY	594	ATTATTTATTTTATTTTATTTTATTTTGAACACAGAGCTCAACTCTGTACCCAGCTGA 653
Db	598	ATTATTTATTTTATTTTATTTTATTTTGAACACAGAGCTCAACTCTGTATCCAGCTGA 656
OY	654	GTCACATGCGCGCAATCTGGCTACATGCACACCTCTGCCGCCGGGTCAAGTATTCGC 713
Db	657	GTCACATGCGCGCAATCTGGCTACATGCACACCTCTGCCGCCGGGTCAAGTATTCGC 716
OY	714	TGCCCGAGGCTCCTAGTAGTGTGGAGTACAGAGGCCCCACACAGCCTTAGTAAATTTTTT 773
Db	717	TGCCCGAGGCTCCTAGTAGTGTGGAGTACAGAGGCCCCACACAGCCTTAGTAAATTTTTT 776
OY	774	GTAATTTTAGTAGAGATGGG - TTCACCATGTGGCAGGTGAATCTTGATCTGTGAC 832
Db	777	GTAATTTTAGTAGAGATGGGTTTACCATGTGGCAGGTGAATCTTGATCTGTGAC 836
OY	833	TTGTGATCTGGCTGCTGGGCT - CCAAAATGCTGGGATTTACAGGCGTACGCCACAG 891
Db	837	TTGTGATCTGGCTGCTGGGCTACCCAAATGCTGGGATTTACAG - GTGTGATCTCAC 894
OY	892	CCCGGCTATTTTATTTTGTGTTGTAATGATCTCACTGTATCCAGGCTG 951
Db	895	GCGGCGCTATTTTATTTTGTGTTGTAATGATCTCACTGTATCCAGGCTG 954
OY	952	GAGTGCATAGGCCAAATCTGAGGCTACATGCACCTGAGCCTCCCGGGCTCAGACGATTC 1011
Db	955	GAGTGCATAGG - CAATCTGGCTACCTGCACACCTTGCCTCCGGG - TCAAGCGATTC 1012
OY	1012	CTGTCTCAGGCTCCCAAGCAGCTGGGATTACGGGCACTGCACACACCCGCTAATT 1071
Db	1013	CTGTCTCAGGCTCCCAAGCAGCTGGGATTACGGG -- ACCTCACACACCCGCTAATT 1070
OY	1072	TTTGTATTTTCAATTAAGAGCGGGGTTCACAAATTTGTGACAGG - GGTCTCAAACTGCT 1130
Db	1071	TTTGTATTTTCAATTAAGAGCGGG - TTTACCAATTTGTGACAGGCTTCAAACTGCT 1128
OY	1131	GACCTCAGGAGACCCACGCTCAGCCTCCAAAGTGTGGATTACAGGCGTAGGCA 1190
Db	1129	GACCTCAGGAGACCCACGCTCAGCCTCCAAAGTGTGGATTACAGGCGTAGGCA 1188
OY	1191	CTCACCCACGCGGCTAATTTAGATAAAAAATATGTAGCAATGGGGGGCTCTGTATGT 1250
Db	1189	CTCACCCACGCGGCTAATTTGTGAATAAAAAATATGTAGCAATGGGG - TCTGTATGT 1246
OY	1251	TGCCCAGGCTGTCTCAAACTCTGGCTTCATGCATCTCTCCAAATAGGACACAGC 1310
Db	1247	TGCCCAGGCTGTCTCAAACTCTGGCTTCATGCATCTCTCCAAATAGGACACAGC 1306
OY	1311	CAGCCAGTCACATTTTAAACAGTTACATCTTATTTAGTACTAGAGAAAGTAAATACA 1370
Db	1307	CAGCCAGTCACATTTTAAACAGTTACATCTTATTTAGTACTAGAGAAAGTAAATACA 1366
OY	1371	ATAAACATGTCAAAC 1385
Db	1367	ATAAACATGTCAAAC 1381







CC treatment of cancer such as colon, breast, stomach, lung, thyroid,  
 CC oesophagal, ovarian, kidney, prostate or pancreatic cancer,  
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,  
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine  
 CC carcinoma, papillary carcinoma and Wilm's tumour.  
 XX

SO Sequence 65608 BP; 15987 A; 16979 C; 16761 G; 15878 T; 3 other;

Query Match 40.8%; Score 587.8; DB 24; Length 65608;  
 Best Local Similarity 70.6%; Pred. No. 5,4e-146;

Matches 940; Conservative 0; Mismatches 347; Indels 44; Gaps 10;

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QY 4 TTTTGTGAGATGAGATTTTCCCTGCTGTTGCCAGCTGAGTGCATAGCCCAATCT 63
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 39993 TTTTGTGAGATGAGATTTT-GCTCTGTGTCAGGCTGAGTGAATAGTGCAGATCT 39935

QY 64 CAGCTCACCAACCTCCGCTCCGCTCCAGCTTCACAGCATTTCTCCCTCAGCTCCAG 123
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 39934 CAGCTCACCAACCTCCGCTCCGCTCCAGCTTCACAGCATTTCTCCCTCAGCTCCAG 39875

QY 124 TACCTGGATTTACAGGATGTCACCCAGCTGCTGCTAATTTTGTATTTTGTAGTAG 183
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 39874 TACCTGGATTTACAGGATGTCACCCAGCTGCTGCTAATTTTGTATTTTGTAGTAG 183

QY 184 AGATGAGATTTTCCAGTGTGTCAGGCTGCTGCTCAGCTCCAGCTCAGATGATCCT 243
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 39818 AGATGAGATTTTCCAGTGTGTCAGGCTGCTGCTCAGCTCCAGCTCAGATGATCCT 39759

QY 244 CCGCTCGGCTCCCAAGTGTAGATATACAGAGCTGCTGCTGCTGCTGCTGCTGCT 303
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 39758 CCGCTCGGCTCCCAAGTGTAGATATACAGAGCTGCTGCTGCTGCTGCTGCTGCT 39700

QY 304 CTAATTTTGTGTAGAAACAGGCTTCTACTGATGTCCTGCTGCTGCTGCTGCTGCT 363
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 39699 AGTATGAAGACATGATCTCCGATATGACAGGCTCCCAACCCAGCTCAGAGACTG 39640

QY 364 AGCAGTCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 403
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 39639 TTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 39580

QY 404 CAGGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 463
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 39579 CCGCTCGGCTCCCAAGTGTAGATATACAGAGCTGCTGCTGCTGCTGCTGCTGCT 39520

QY 464 TCTTACCCAGATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 523
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 39519 TCTTACCCAGATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 39460

QY 524 GATC-AAGCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 582
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 39459 GCTCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 39400

QY 583 ACACCTGCTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 642
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 39399 ATGCCCACTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 39348

QY 643 CCAAGGCTGAGTGCAGTGGGCAATCTTGGCTCAGTCAACCTGCTGCTGCTGCTGCTGCT 702
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 39347 CCAAGGCTGAGTGCAGTGGGCAATCTTGGCTCAGTCAACCTGCTGCTGCTGCTGCTGCT 39288

QY 703 AGTATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 762
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 39287 AGTATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 39228

QY 763 CTAATTTTGTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 821
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 39227 TGGCTAATTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 39168

QY 822 ATCTCTGACCT--TGATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 879
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 39167 AACTCTGACCTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 39108

QY 880 TGAGCCACGACGCGCGCTT--ATTTTAAATTTTGTGTTGTAATAATGAAATCTACTCT 937

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DB 39107 TGAGCCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 39048
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 938 TGTTACCAGGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 997
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 39047 TGTTACCAGGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 38988

QY 998 GCTCAAGGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1057
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 38987 GCTCAAGGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 38928

QY 1058 ACACCCGCTAATTTTGTATTTTGTATTTTGTATTTTGTATTTTGTATTTTGTATTTTGT 1117
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 38927 ACAGCCGCTAATTTTGTATTTTGTATTTTGTATTTTGTATTTTGTATTTTGTATTTTGT 38868

QY 1118 GTCTCAAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1177
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 38867 GTCTCAAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 38808

QY 1178 CAGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1233
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 38807 CAGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 38748

QY 1234 GGGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1293
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 38747 ACAGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 38688

QY 1294 AATGAGCCAC 1304
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 38687 GTCTCAAGCTCT 38677

RESULT 7
AB167668/C
ID AB167668 standard; DNA; 65608 BP.
XX
AC AB167668;
XX
DT 15-MAY-2002 (first entry)
XX
DE Oesophagus cancer related gene sequence SEQ ID NO:6005.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PR 30-MAY-2001; 2001WO-US10838.
XX
PR 05-JUN-2000; 2000US-209473P.
PR 05-JUN-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234509P.
PR 22-SEP-2000; 2000US-234567P.
PR 25-SEP-2000; 2000US-234923P.
PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 26-SEP-2000; 2000US-235638P.
PR 27-SEP-2000; 2000US-235711P.

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CC an anti-neoplastic agent, and can be used for producing a product which  
 CC is the data collected with respect to the anti-neoplastic agent as a  
 CC result of M1, and the data is sufficient to convey the chemical  
 CC structure and/or properties of the agent. M1 can be used in the  
 CC treatment of cancer such as colon, breast, stomach, lung, thyroid,  
 CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,  
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,  
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine  
 CC carcinoma, papillary carcinoma and Wilms' tumour.

XX Sequence 62944 BP: 15145 A; 17344 C; 15900 G; 14555 T; 0 other:

Query Match 36.4%; Score 524.4; DB 24; Length 62944;

Best Local Similarity 71.9%; Pred. No. 4.3e-129;

Matches 963; Conservative 0; Mismatches 321; Indels 56; Gaps 19;

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QY 1 TTTTATTTTATTTAGATTTGAGTTTGGCTTTGTTGCCAGGCTGAGTGCATTTGGCGCAA 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 59357 TATTTATTTTGGATGAGTGGTTT-GCTCTCTCGCCAGGCTGAGTGCAGTGGCGCAA 59415
QY 61 TCTCAGCTACCGCAACCTCCGCTCCCGGTTCAAGAGTATCTCCGCTCCGCTCCGCTCC 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 59416 TCTGCTCTACAGCAACCTCCGCTCTCTAGTTCAATGATTTCTCTGCTCCAGCT-- 59472
QY 121 CAGTACGTGGATTACAGGATGTGCACCCACGCTGCTAATTTTGTATTTTATTTAG 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 59473 TAGTAGGTGTATTACAGGATCTGCACACGCCACGCTAATTTT--TGATTTTATAC 59529
QY 181 TAGAGATGAGTTCTCATGTTGTCAGGCTGTCTGCAACTCCGACCTCAGATGATC 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 59530 TAGAGACAGGTTTACCATGTGGCGAGGCTGTGTGAACCTCGATCTAAGGTTATC 59589
QY 241 CCTCGCTCGGCTCCCAAGTCTAG---ATACAGAGCTGCGCACCATCGCCGCTC 296
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 59590 TGCTTACCTCGGCTCCCAAGTCTGAGATTACACAGCTGAGCCAGCCAGCCACCTC 59649
QY 297 TGCCTGGCTAT-TTTTGTGTAGAAACAGGTTTCACTGATGTGCCAAGCTGTCTCC 355
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 59650 TTTTCTTTTCTTTTCTTTTCTTGTGAGGAGGCTCTGCTGTCCACCGCTGAGTGC 59709
QY 356 TG---AGCTCAGACAGTCCACCTGCTCAGCTCCCAAGTGTGGGATTACAGGCGTG 411
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 59710 AGCAGCAGGATCATAGCTACATGAGCTTCGATCTCCGCTCAAGTATCTCCAGCT 59769
QY 412 CAGCCGCTGCTTTTATTTTATTTTATTTTAAAGACAGTGTCCACTCTTACC 471
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 59770 AATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 59828
QY 472 AGGATGAGGATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 531
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 59829 AGACTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 59887
QY 532 ATCTCTCTGCTCAGCTCCCAAGTGTGATGATGATGATGATGATGATGATGATG 591
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 59888 AATTTCTGCTCAGCTCCCAAGTGTGATGATGATGATGATGATGATGATGATG 59946
QY 592 TAAATTTTAA-TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 649
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 59947 TAAATTTTGGGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 60005
QY 650 TGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 709
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 60006 TGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60065
QY 710 CTCTGCTCC-----CAGCTCTCTGATGATGATGATGATGATGATGATGATG 759
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 60066 CTCTGCTCC-----CAGCTCTCTGATGATGATGATGATGATGATGATGATG 60125
QY 760 TAGCTAAT---TTTTGTATTTTATTTATTTATTTATTTATTTATTTATTTATTT 815
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 60126 CAGTTAATTTTGTATTTTATTTTATTTATTTATTTATTTATTTATTTATTTATTT 60185
QY 816 AATCTGATCTGTGACCTGTGATCTGTGCTCGGCTCCCAAGTGTGATGATGATG 875

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Db 60186 GTCTCAATCTCTGACCTGTGTATCTCGCTCTCACTCCCAAGTGTGATGATGATG 60245
QY 876 GAGCTGACCAACCAAGCCCGGCTATTT-----TTTAAATTTTGTGTGTAAT 925
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 60246 GCGTTGAGCAACCGCCCTGGCTGTTTGTGTGTTTGTGTGTTTGTGTGTTTGTGTG 60305
QY 926 GGAATCTACTCTGTATCCAGGCTGAGTGAATGGCCAAATCTGCTCACTGCAACC 985
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 60306 GAATTTGCTCTGTGTGCTCAAGCTGAGTGAATGGCTGATGATGATGATGATGATG 60365
QY 986 TCTGCTCCCGGCGGCAAGCATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1045
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 60366 TCTGCTCCCGGCTGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60425
QY 1046 GCACCTGCAACCAACCCCGCTAA-TTTTGTATTTTATTTATTTAGAGGCGGTTACCAT 1104
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 60426 GCGTGTGCCACATGCGCGGCTAATTTTGTATTTTATTTATTTAGTAATGAGGTTTACCAT 60485
QY 1105 ATTTGTACGCTGTGTCTAAACTCTGACCTGACCTGACCTGCTGCTGCTGCTGCTG 1164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 60486 ATTTGTACGCTGTGTCTAAACTCTGACCTGACCTGACCTGCTGCTGCTGCTGCTG 60543
QY 1165 AGTCTGGATTTACAGGCGTGTGAGCACTCAACCCAGCGGCTAATTTATGATTAATAATA 1224
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 60544 AGTCTGGATTTACAGGCTGTGATGATGATGATGATGATGATGATGATGATGATG 1284
QY 1225 TGTAGCAATGGGCGGCTGTGTGATGATGATGATGATGATGATGATGATGATGATG 1284
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 60597 TTAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60656
QY 1285 AATCTTCCAAATGAGGCTAC 1304
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 60657 AATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60676

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RESULT 10  
 AAK69279/c  
 ID AAK69279 standard; DNA: 33747 BP.

XX AAK69279;

XX 06-NOV-2001 (first entry)

XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24091.

XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
 KW cytosolic; gene therapy; vaccine; metastasis; ds.

XX Homo sapiens.

XX MO200157182-A2.

XX 09-AUG-2001.

XX 17-JAN-2001; 2001WO-US01354.

XX 31-JAN-2000; 2000US-0179065.

XX 04-FEB-2000; 2000US-0180628.

XX 24-FEB-2000; 2000US-0184664.

XX 02-MAR-2000; 2000US-0186350.

XX 16-MAR-2000; 2000US-019874.

XX 17-MAR-2000; 2000US-019076.

XX 18-APR-2000; 2000US-0198123.

XX 19-MAY-2000; 2000US-020515.

XX 07-JUN-2000; 2000US-0209467.

XX 28-JUN-2000; 2000US-0214886.

XX 30-JUN-2000; 2000US-0215135.

XX 07-JUL-2000; 2000US-0216647.

XX 07-JUL-2000; 2000US-0216880.

XX 11-JUL-2000; 2000US-0217487.

XX 11-JUL-2000; 2000US-0217496.

XX 14-JUL-2000; 2000US-0218290.







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Db 541 TTTTTCCTTTTGTAGATGAGTCT--CGCTCTGTGCGCCAGGTTGGAGTGCAGTATGTA 598
Qy 61 TCTCAGCTCACCACCAACCTCCGCTCCCGGTTTCAAGCATTTCTGCTCAGCGCTCC 120
Db 599 TCTCAGCTCAGTACCAACCTCCGCTCCCGGTTTCAAGCATTTCTGCTCAGCGCTCC 658
Qy 121 CAGTACGCTGGATTTACAGGATGTCACCCAGCTCGCGCTAAATTTTGTATTTTGTAG 180
Db 659 TAGAAGCTGGGATTTATAGCCCTGCACACCATGCTGCTAATTTT--TGTATTTTNG 715
Qy 181 TAGAGATGAGATTTTCTCATGTTGGTGGGCTGCTGCAACTCCCGAGCTCAGATGATC 240
Db 716 CAGAGACGGGGTTTGGCATGTTGGCCAGGCTGGTCTCAAACTCTGAACTCAGGTGATC 775
Qy 241 CCTCCCTCTCGGCTCCCAAGTGTCTAGATACAGGACTGGCCACCATCCCGGCTCTGCC 300
Db 776 TGCCTGGCTTGGCTCCCAAGTGTCTAGATTTACAGTTGTAGCCACATGCACTTGGCTA 835
Qy 301 TGGCTAATTTTGTGTGTAAGAAACAGGGTTTCACTGATGTGCCCAAGTGTCTCTC---- 355
Db 836 TTTTTCCTTTTGTGTGTAAGAAACAGGGTTTCACTGATGTGCCCAAGTGTCTCTC---- 355
Qy 356 TGAGCTCAAGCAGTCCACCTCCTCAGCTCCCAAGTGTGGGATTTACAGGCTGTCAGC 415
Db 896 TATGATCAGCTCATGTCAGCTCCCAAGTGTGGGATTTACAGGCTGTCAGC 955
Qy 416 CGTGCTGCTCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 475
Db 956 TGCCTGATGCTGCTGGGCTTACCAAGTGTGGGATTTATGAGCATGTGTCAGATTTT 1015
Qy 476 TGAAGTACAGTGTGTGATCA--CAGCTCAGTGCAGCTTCACTCCTGCAATATGATCAAG-A 532
Db 1016 TGTGATGATGAGGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1075
Qy 533 TCTCTGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCT 592
Db 1076 TCTCTGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCT 1135
Qy 593 AATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 652
Db 1136 TATATCAT-TGGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1193
Qy 653 AGTACAGTGGGCAATCTGCTCAGTCACTGCAACCTGCTCCCGGCTTCAAGTATTTCTC 712
Db 1194 AGTACAGTGGGCAATCTGCTCAGTCACTGCAACCTGCTCCCGGCTTCAAGTATTTCTC 1253
Qy 713 CTGCTCAGCTCCTCTGAGTGTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 769
Db 1254 CTGCTCAGCTCCTCTGAGTGTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1313
Qy 770 TTTTGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 829
Db 1314 TTTTGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1373
Qy 830 ACCTTGTGATCTGCTGCTCAGTGTGCTCAGTGTGCTCAGTGTGCTCAGTGTGCTCAGT 889
Db 1374 ACCTTGTGATCTGCTGCTCAGTGTGCTCAGTGTGCTCAGTGTGCTCAGTGTGCTCAGT 1433
Qy 890 CCGCGGCTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 949
Db 1434 CACCGGCTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1492
Qy 950 TGGAGTCAATGAGGCAATCTGCTGCTCAGTGTGCTCAGTGTGCTCAGTGTGCTCAGTGT 1009
Db 1493 TGGAGTCAATGAGGCAATCTGCTGCTCAGTGTGCTCAGTGTGCTCAGTGTGCTCAGTGT 1552
Qy 1010 CTCTGCTCAGCTCCTCAGTGTGCTCAGTGTGCTCAGTGTGCTCAGTGTGCTCAGTGTGCT 1069
Db 1553 TTTCTGCTCAGCTCCTCAGTGTGCTCAGTGTGCTCAGTGTGCTCAGTGTGCTCAGTGTGCT 1612
Qy 1070 TTTTGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1129
Db 1613 TTTTGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1672

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Qy 1130 TGACCTCAGCTGATCCACCTGCTCAGCTTCCAAAGTGTGGATTTACAGGCTGAGCC 1189
Db 1673 TGACCTTAACTGATCTGCGCTCAGCTCCCAAGTGTGGATTTACAGGATGAGCC 1732
Qy 1190 ACCTCAGCCAGCGGCTAATTTAGAT 1215
Db 1733 ACTGTGCTGGCCATTGACTTTTAT 1758

RESULT 12
ABK85018/C
ID ABK85018 standard; DNA; 43545 BP.
XX
XX ABK85018;
XX
XX 13-AUG-2002 (first entry)
XX
XX
XX Human cadherin-like asymmetry protein-2 (CLASP-2) genomic DNA.
XX
XX Human; autoimmune disease; haematopoietic disorder; Digorge syndrome;
XX blood protein disorder; agammaglobulinaemia; dysgammaglobulinaemia;
XX ataxia telangiectasia; common variable immunodeficiency; lymphopenia;
XX thrombocytopenia; haemoglobinuria; Addison's disease; Graves' disease;
XX haemolytic anaemia; multiple sclerosis; rheumatoid arthritis; lupus;
XX endometriosis; autoimmune thyroiditis; anaphylaxis; hypersensitivity;
XX autoimmune pulmonary inflammation; organ rejection; inflammation;
XX CLASP; gene; ds.
XX
XX Homo sapiens.
XX
XX WO20023117-A2.
XX
XX 18-Apr-2002.
XX
XX 15-OCT-2001; 2001WO-US32202.
XX
XX 13-OCT-2000; 2000US-0687837.
XX
XX (ARBO-) ARBOR VITA CORP.
XX (GARM-) GARMAN J D.
XX (CAND-) CANDIA A F.
XX
XX Lu PS;
XX
XX WPI; 2002-416861/44.
XX
XX New human cadherin-like asymmetry protein(s) (CLASP)-2 for modulating
XX an immune response, and for treating multiple sclerosis, rheumatoid
XX arthritis, endometriosis, lupus, autoimmune thyroiditis, septic shock,
XX and sepsis.
XX
XX Disclosure; Figure 12B; 245pp; English.
XX
XX The invention relates to an isolated polypeptide (I) comprising an amino
XX acid sequence that has 90 % sequence identity to one of the human
XX cadherin-like asymmetry protein(s) (CLASP)-2 (hCLASP-2B, 2C, 2E)
XX sequences (PS). (I) is useful for identifying a compound or agent that
XX binds CLASP-2 polypeptide. An antibody (II) to (I) is useful for
XX detecting a CLASP-2 polypeptide in a sample. (II) is useful for
XX inhibiting a immune response in a subject. A pharmaceutical composition
XX comprising a nucleic acid encoding (I), or (II) is useful for preventing
XX or treating a CLASP-2 mediated disease e.g. an autoimmune disease, where
XX the autoimmune disease is caused or exacerbated by increased activity
XX of TH1 cells. CLASP-2 polynucleotides are useful as probes or primers for
XX detection or inhibition of CLASP-2 expression (e.g., antisense or
XX ribozyme-mediated inhibition), for gene knockout, etc. The CLASP-2
XX polynucleotides can express CLASP-2 polypeptides, produce anti-CLASP-
XX antibodies or are used as therapeutic polypeptides. The CLASP-2
XX polynucleotide or fragments can be used in diagnostics (e.g., as probes
XX for CLASP-2 expression), as a lymphocyte marker and for therapeutic
XX purposes. CLASP-2 polynucleotides can construct transgenic and knockout
XX animals, e.g., for screening of CLASP-2 agonists and antagonists. CLASP-2

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PR 16-MAR-2000; 2000US-0189874.  
 PR 17-MAR-2000; 2000US-0190076.  
 PR 18-APR-2000; 2000US-0198123.  
 PR 19-MAY-2000; 2000US-0205515.  
 PR 07-JUN-2000; 2000US-0209467.  
 PR 28-JUN-2000; 2000US-0214886.  
 PR 30-JUN-2000; 2000US-0215135.  
 PR 07-JUL-2000; 2000US-0216647.  
 PR 11-JUL-2000; 2000US-0216880.  
 PR 11-JUL-2000; 2000US-0217487.  
 PR 14-JUL-2000; 2000US-0217496.  
 PR 26-JUL-2000; 2000US-0220963.  
 PR 26-JUL-2000; 2000US-0220964.  
 PR 14-AUG-2000; 2000US-0224518.  
 PR 14-AUG-2000; 2000US-0224519.  
 PR 14-AUG-2000; 2000US-0225213.  
 PR 14-AUG-2000; 2000US-0225214.  
 PR 14-AUG-2000; 2000US-0225266.  
 PR 14-AUG-2000; 2000US-0225267.  
 PR 14-AUG-2000; 2000US-0225268.  
 PR 14-AUG-2000; 2000US-0225270.  
 PR 14-AUG-2000; 2000US-0225447.  
 PR 14-AUG-2000; 2000US-0225757.  
 PR 14-AUG-2000; 2000US-0225758.  
 PR 18-AUG-2000; 2000US-0225759.  
 PR 22-AUG-2000; 2000US-0226279.  
 PR 22-AUG-2000; 2000US-0226681.  
 PR 22-AUG-2000; 2000US-0226682.  
 PR 23-AUG-2000; 2000US-0227009.  
 PR 30-AUG-2000; 2000US-0228924.  
 PR 01-SEP-2000; 2000US-0229287.  
 PR 01-SEP-2000; 2000US-0229343.  
 PR 01-SEP-2000; 2000US-0229344.  
 PR 05-SEP-2000; 2000US-0229345.  
 PR 05-SEP-2000; 2000US-0229509.  
 PR 06-SEP-2000; 2000US-0229513.  
 PR 06-SEP-2000; 2000US-0230433.  
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 PR 02-OCT-2000; 2000US-0237039.  
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 PR 08-DEC-2000; 2000US-0251869.  
 PR 08-DEC-2000; 2000US-0251989.  
 PR 11-DEC-2000; 2000US-0251990.  
 PR 05-JAN-2001; 2001US-0259678.  
 (HUMA-) HUMAN GENOME SCI INC.  
 Rosen CA, Barash SC, Ruben SM,  
 WPI, 2001-565190/63.  
 PT Nucleic acid encoding novel connective tissue associated polypeptides,  
 PT used in diagnosing, preventing, treating or ameliorating a disorder  
 XX such as cancer or rheumatoid arthritis.  
 PS Disclosure; SEQ ID No 1157; 673pp; English.  
 CC The present invention relates to the isolation of novel human connective



PR 14-AUG-2000; 2000US-0225267.  
 PR 14-AUG-2000; 2000US-0225268.  
 PR 14-AUG-2000; 2000US-0225270.  
 PR 14-AUG-2000; 2000US-0225447.  
 PR 14-AUG-2000; 2000US-0225757.  
 PR 14-AUG-2000; 2000US-0225758.  
 PR 18-AUG-2000; 2000US-0225759.  
 PR 22-AUG-2000; 2000US-0226279.  
 PR 22-AUG-2000; 2000US-0226681.  
 PR 22-AUG-2000; 2000US-0227182.  
 PR 23-AUG-2000; 2000US-0227009.  
 PR 30-AUG-2000; 2000US-0228924.  
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PR 08-NOV-2000; 2000US-0246526.  
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 PR 08-DEC-2000; 2000US-0251989.  
 PR 11-DEC-2000; 2000US-0251990.  
 PR 05-JAN-2001; 2000US-0259678.

(HUMA-) HUMAN GENOME SCI INC.  
 Rosen CA, Barash SC, Ruben SM;  
 WPL: 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
 useful for preventing, diagnosing and/or treating cancers and  
 metastasis -  
 Disclosures: SEQ ID NO 26580; 3071pp + Sequence Listing; English.  
 AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)  
 amino acid sequences given in AAK62170 to AAK91921. (I) have cytostatic  
 activity, and can be used in gene therapy and vaccine production. (I)  
 proteins and polynucleotides may be used in the prevention, diagnosis and  
 treatment of diseases associated with inappropriate (I) expression. For  
 example, they may be used to treat disorders associated with decreased  
 expression by rectifying mutations or deletions in a patient's genome  
 that affect the activity of (I) by expressing inactive proteins or to  
 supplement the patients own production of (I). Additionally, (I)  
 polynucleotides may be used to produce the secreted (I), by inserting  
 the nucleic acids into a host cell and culturing the cell to express the  
 protein. (I) proteins and polynucleotides may be used to prevent,  
 diagnose and treat immune/haematopoietic-related diseases, especially  
 cancers and cancer metastases of haematopoietic-derived cells. AAK64703  
 to AAK87694 represent human immune/haematopoietic antigen genomic  
 sequences from the present invention. AAK54942 to AAK54950 and AAK87169  
 represent sequences used in the exemplification of the present invention.

Sequence 5262 BP; 1099 A; 1347 C; 1247 G; 1569 T; 0 other.



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PR	29-SEP-2000	2000US-0236368	DR	WPI; 2001-483426/52.	
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PR	29-SEP-2000	2000US-0236370	PT	Nucleic acids encoding human immune/hematopoietic antigen polypeptides,	
PR	02-OCT-2000	2000US-0236802	PT	useful for preventing, diagnosing and/or treating cancers and	
PR	02-OCT-2000	2000US-0237037	XX	metastasis -	
PR	02-OCT-2000	2000US-0237038	XX		
PR	02-OCT-2000	2000US-0237039	PS	Disclosure; SEQ ID NO 26581; 3071pp + Sequence listing; English.	
PR	02-OCT-2000	2000US-0237040	XX		
PR	13-OCT-2000	2000US-0239335	CC	AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)	
PR	13-OCT-2000	2000US-0239337	CC	amino acid sequences given in <i>AM82170</i> to <i>AAK91921</i> . (I) have cytostatic	
PR	20-OCT-2000	2000US-0240960	CC	activity, and can be used in gene therapy and vaccine production. (I)	
PR	20-OCT-2000	2000US-0241221	CC	proteins and polynucleotides may be used in the prevention, diagnosis and	
PR	20-OCT-2000	2000US-0241785	CC	treatment of diseases associated with inappropriate (I) expression. For	
PR	20-OCT-2000	2000US-0241786	CC	example, they may be used to treat disorders associated with decreased	
PR	20-OCT-2000	2000US-0241787	CC	expression by rectifying mutations or deletions in a patient's genome	
PR	20-OCT-2000	2000US-0241808	CC	that affect the activity of (I) by expressing inactive proteins or to	
PR	20-OCT-2000	2000US-0241809	CC	supplement the patients own production of (I). Additionally, (I)	
PR	01-NOV-2000	2000US-0244617	CC	polynucleotides may be used to produce the secreted (I), by inserting	
PR	08-NOV-2000	2000US-0246474	CC	the nucleic acids into a host cell and culturing the cell to express the	
PR	08-NOV-2000	2000US-0246475	CC	protein. (I) proteins and polynucleotides may be used to prevent,	

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 Db 1500 CAGTAGCTGGATTACAGGACGTCACGACCATGCCAGCTTATTTT--TGTATTTTGG 1556  
 QY 181 TAGAGATGAGATTTCACATGTTGTCAGGCTGGTTCGAACTCCGAGCTCAGATGATC 240  
 Db 1557 TAGAGAGGCGGTTCCACCATGTTGACACAGGCTGGTTCGAACTCCGAGCTCAGATGATC 1616  
 QY 241 CCTCGCTCCGCGCTCCCAAGATGCTAGATACAGGACTGGCCACCATGCCGCGCTGCC 300  
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 QY 361 TCAGAGATCCACCTGCTCAGGCTCCCAAGTGTGGGATTTACAGGCGCTGACCGCTGC 420  
 Db 1729 ----- 1728  
 QY 421 CTGGCCTTTTATTTTATTTTATTTTAAAGACAGAGTGTCCACTCTTACCAGATGAAG 480  
 Db 1729 -TTCTTCTTTTATTTTATTTTATTTTAAAGACAGAGTGTCCACTCTTACCAGATGAAG 1787  
 QY 481 TGCAGTGTGTGATCAGAGCTCAGCTCAGGCTTCACTCCTGATCAAG-CAWCTCCT 539  
 Db 1788 GACAGTGTGATGATGACGACTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCT 1847  
 QY 540 GCTCAGCTCCCAAGTACGCTGGGACCAAGATGACACCATACACTGCTGCTAATTTT 599  
 Db 1848 GCTCAGCTCCCAAGTACGCTGGGATTTACAGGATGACACCATACACTGCTGCTAATTTT 1907  
 QY 600 ATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 659  
 Db 1908 -TGTGTTGTTTGTGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1965  
 QY 660 TGGCGCAATCTTGGCTCACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 719  
 Db 1966 TGGCGCAATCTTGGCTCACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2025  
 QY 720 AGCTCCTGAGTACGCTGAGCTACAGCGGCCCAAGGCTGCTGCTGCTGCTGCTGCTGCT 778  
 Db 2026 AGCTCCTGAGTACGCTGAGCTACAGCGGCCCAAGGCTGCTGCTGCTGCTGCTGCTGCT 2085  
 QY 779 TTTAGTAGATGAGG-TTACCATGTTGCGGATGATCTTGTGATCTGTGACCT--TG 835  
 Db 2086 TTTAGTAGATGAGG-TTACCATGTTGCGGATGATCTTGTGATCTGTGACCT--TG 835  
 QY 836 TGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 895  
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Search completed: February 1, 2003, 21:37:50  
 Job time : 605 secs





GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 20:06:24 ; Search time 3874 Seconds

(without alignments)  
10832.795 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: gb\_in:\*  
4: gb\_lm:\*  
5: gb\_ov:\*  
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7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rod:\*  
36: em\_htg\_mam:\*  
37: em\_htg\_vrt:\*  
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40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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5	1301.4	90.2	124001	9 HS886K2	AL031295 Human DNA
6	1080.2	74.9	1381	6 AR051479	AR051479 Sequence
7	1080.2	74.9	1381	6 AR072619	AR072619 Sequence
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#### ALIGNMENTS

RESULT 1  
LOCUS AR051550 1442 bp DNA  
DEFINITION Sequence 120 from patent US 5830670.  
ACCESSION AR051550  
VERSION AR051550.1 GI:5974914  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1442)  
AUTHORS de la Monte,S. and Wands,J.R.  
TITLE Neural thread protein gene expression and detection of Alzheimer's disease  
JOURNAL Patent: US 5830670-A 120 03-NOV-1998;



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Oy	361	TCAAGCAGTCCACCTGGCTCAGCGCTCCCAAGTGTGGATTACAGGCGTGAAGCCGCTGC	420
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QY	1261	GGTCTCAAACTCTGTGCTTCATGCATCCTTCCAAATGAGCCACCAACCCAGCCAGTCA	1320
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Db	1441	CA 1442	
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DEFINITION	Sequence 120 from patent US 5948888.	linear	PAT 28-AUG-2000
ACCESSION	AR073235		
VERSION	AR073235.1	GI:9999998	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1442)		
TITLE	de la Monte,S., and Wands,J.R.		
FEATURES	Neural thread protein gene expression and detection of Alzheimer's disease		
Journal	Patent: US 5948888-A 120 07-SEP-1999;		
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Best Local Similarity	100.0%; Pred. No. 0;		
Matches 1442; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
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LOCUS AF010144 1442 bp mRNA linear PRI 02-NOV-2001
DEFINITION Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds.
ACCESSION AF010144
VERSION AF010144.1 GI:3002526
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 1442)
AUTHORS Monte, S.W., Ghanbari, K., Frey, W.H., Beheshti, I., Averbach, P.,
Hauser, S.L., Ghanbari, H.A., and Wands, J.R.
TITLE Characterization of the AD7c-NTP cDNA expression in Alzheimer's
disease and measurement of a 41-kD protein in cerebrospinal fluid
JOURNAL J. Clin. Invest. 100 (12), 3093-3104 (1997)
MEDLINE 98064067
PUBMED 9399956
REFERENCE 2 (bases 1 to 1442)
AUTHORS de la Monte, S.M., and Wands, J.R.
TITLE Direct Submission
JOURNAL Submitted (24-JUN-1997) MGH Cancer Center, Massachusetts General
Hospital, 149 13th Street, Room 7308, Charlestown, MA 02129, USA
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Best Local Similarity 100.0%; Pred. No. 0;
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QY	1441	CA 1442	

Db 1441 CA 1442

RESULT 5  
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LOCUS  
DEFINITION  
124001 bp DNA linear PRI 23-NOV-1999  
Human DNA sequence from clone 886K2 on chromosome 1p35.1-36.12  
Contains elongin A (RNA polymerase II elongation factor),  
hydroxymethylglutaryl-CoA lyase, GALE (UDP-galactose-4-epimerase)  
ESTs, GSS, STS, Cpg island, complete sequence.  
AL031295  
AL031295.1 GI:4376011  
HG: Cpg island; elongin A; GALE; HMGCL; hydroxymethylglutaryl-CoA  
lyase; RNA polymerase II elongation factor.  
SOURCE  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Direct Submission  
Submitted (20-APR-1999) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
Requests: clonequests@sanger.ac.uk  
On Mar 7, 1999 this sequence version replaced gi:4056542.  
During difference assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variation annotation may not be found in the sequence submission  
corresponding to the overlapping clone, as we submit sequences with  
only a small overlap as described above.  
This sequence is the entire insert of clone 886K2. This sequence  
has been finished according to sequence map criteria as follows. An  
attempt is made to resolve all sequencing problems, such as  
compressions and repeats, but not necessarily within known  
annotated human repeat sequence elements (e.g. Alu). Where the  
sequence is ambiguous, there is an annotation using the 'unsure'  
feature key.  
This sequence was generated from part of bacterial clone contigs of  
human chromosome 1, constructed by the Sanger Centre Chromosome 1  
Mapping Group. Further information can be found at  
http://www.sanger.ac.uk/HGP/Chr1  
886K2 is from the library RRC15 constructed at the Roswell Park  
Cancer Institute by the group of Pieter de Jong. For further  
details see http://bacpac.med.buffalo.edu/VECTOR: pcrpac2.  
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1671. 1848  
/note="MIR repeat: matches 67. 261 of consensus"  
complement(<1849. >2287)  
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match: A1276680 AA232246 AA525120 AA032081 A1275142"  
2288. 2429  
repeat\_region

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/note="AluIo/FRAM repeat: matches 157. .300 of consensus"
2430. .2714
repeat_region /note="AluSq repeat: matches 1. .287 of consensus"
2728. 3063
repeat_region /note="L1M4 repeat: matches 2200. .2535 of consensus"
3385. .3686
repeat_region /note="AluSx repeat: matches 1. .310 of consensus"
3709. .4050
repeat_region /note="PHEIC repeat: matches 1. .371 of consensus"
4064. .4212
repeat_region /note="FRAM repeat: matches 1. .155 of consensus"
4358. .4506
repeat_region /note="MER5A repeat: matches 15. .182 of consensus"
4788. .4878
repeat_region /note="AluIo repeat: matches 54. .149 of consensus"
4879. .5178
repeat_region /note="AluSx repeat: matches 1. .302 of consensus"
5181. .5484
repeat_region /note="AluSg repeat: matches 1. .305 of consensus"
5485. .5653
repeat_region /note="AluIo repeat: matches 149. .304 of consensus"
5654. .5788
repeat_region /note="AluSx repeat: matches 1. .132 of consensus"
5789. .6089
repeat_region /note="AluSp repeat: matches 1. .297 of consensus"
6090. .6260
repeat_region /note="AluSx repeat: matches 132. .312 of consensus"
6282. .6580
repeat_region /note="AluY repeat: matches 1. .296 of consensus"
6596. .7224
repeat_region /note="L2 repeat: matches 1995. .2748 of consensus"
7225. .7293
repeat_region /note="AluIb repeat: matches 152. .220 of consensus"
7294. .7753
repeat_region /note="L2 repeat: matches 1543. .1995 of consensus"
7756. .8048
repeat_region /note="AluSg repeat: matches 1. .279 of consensus"
8050. .8358
repeat_region /note="AluY repeat: matches 1. .309 of consensus"
8420. .8987
repeat_region /note="L2 repeat: matches 873. .1539 of consensus"
8998. .9090
repeat_region /note="L2 repeat: matches 1543. .1627 of consensus"
9060. .9105
repeat_region /note="L2 repeat: matches 827. .872 of consensus"
9180. .9279
repeat_region /note="MIR repeat: matches 35. .139 of consensus"
9489. .9671
repeat_region /note="MER5A repeat: matches 1. .189 of consensus"
10046. .10047
repeat_region /note="Random repeat. Region of tandem repeat each element
48 base pairs and typical sequence:
GAAGAGCTGTAGATTATATACATCCCTTGAGTTCG
Restriction digest information (HINDIII) suggests 3 copies
of the repeat are missing from this assembly."
10530. .10594
repeat_region /note="L2 repeat: matches 2676. .2750 of consensus"
10604. .10678
repeat_region /note="MIR repeat: matches 12. .87 of consensus"
11227. .11408
repeat_region /note="MIR repeat: matches 20. .232 of consensus"
11470. .11776
repeat_region /note="AluSg repeat: matches 1. .311 of consensus"
12244. .12546
repeat_region /note="AluY repeat: matches 1. .303 of consensus"
13021. .13318
repeat_region /note="AluSx repeat: matches 1. .295 of consensus"
13319. .13389
repeat_region /note="MER5A repeat: matches 73. .137 of consensus"
13390. .13685
repeat_region /note="AluSg repeat: matches 1. .297 of consensus"
13686. .13730
repeat_region /note="MER5A repeat: matches 27. .73 of consensus"
13759. .13823
repeat_region /note="L2 repeat: matches 2146. .2215 of consensus"
13824. .13959
repeat_region /note="FLAM_A repeat: matches 1. .133 of consensus"
13960. .14115
repeat_region /note="L2 repeat: matches 2012. .2146 of consensus"
14221. .14479
repeat_region /note="MER1B repeat: matches 156. .456 of consensus"
14660. .14709
repeat_region /note="MIR repeat: matches 49. .98 of consensus"
14953. .15263
repeat_region /note="AluSx repeat: matches 1. .311 of consensus"
15508. .15684
repeat_region /note="MIR repeat: matches 2. .218 of consensus"
15724. .15857
repeat_region /note="FLAM_A repeat: matches 1. .133 of consensus"
15961. .16086
repeat_region /note="FAM repeat: matches 12. .163 of consensus"
16087. .16394
repeat_region /note="AluSg repeat: matches 3. .310 of consensus"
16395. .16409
repeat_region /note="FAM repeat: matches 163. .174 of consensus"
16722. .16804
repeat_region /note="L2 repeat: matches 2582. .2691 of consensus"
16908. .17483
repeat_region /note="L1MB3 repeat: matches 5598. .6185 of consensus"
17679. .17881
repeat_region /note="L2 repeat: matches 2285. .2490 of consensus"
18516. .18927
repeat_region /note="MLTID repeat: matches 114. .505 of consensus"
18928. .19043
repeat_region /note="FLAM_C repeat: matches 1. .116 of consensus"
19044. .19149
repeat_region /note="MLTID repeat: matches 6. .114 of consensus"
19750. .20088
repeat_region /note="L2 repeat: matches 2273. .2646 of consensus"
20092. .20153
repeat_region /note="31 copies 2 mer aa 81% conserved"
20170. .20479
repeat_region /note="AluSx repeat: matches 3. .312 of consensus"
20499. .20633
repeat_region /note="L2 repeat: matches 2623. .2750 of consensus"
20639. .20946
repeat_region /note="AluSx repeat: matches 1. .308 of consensus"
20959. .21232
repeat_region /note="AluIb repeat: matches 1. .297 of consensus"
21240. .21532
repeat_region /note="AluSg repeat: matches 1. .293 of consensus"
21534. .21837
repeat_region /note="AluSp repeat: matches 2. .310 of consensus"
21839. .21936
repeat_region /note="MER5B repeat: matches 84. .175 of consensus"
21952. .22283
repeat_region /note="L2 repeat: matches 1811. .2198 of consensus"
22303. .22605
repeat_region /note="AluY repeat: matches 1. .301 of consensus"
22665. .22969
repeat_region /note="AluSg repeat: matches 1. .304 of consensus"
23308. .23605
repeat_region /note="AluSp repeat: matches 1. .298 of consensus"
13759. .13823
repeat_region /note="L2 repeat: matches 2146. .2215 of consensus"
13824. .13959
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20639. .20946
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21240. .21532
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repeat_region /note="MER5B repeat: matches 84. .175 of consensus"
21952. .22283
repeat_region /note="L2 repeat: matches 1811. .2198 of consensus"
22303. .22605
repeat_region /note="AluY repeat: matches 1. .301 of consensus"
22665. .22969
repeat_region /note="AluSg repeat: matches 1. .304 of consensus"
23308. .23605
repeat_region /note="AluSp repeat: matches 1. .298 of consensus"
Query Match 90.2%; Score 1301.4; DB 9; Length 124001;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1409; Conservative 0; Mismatches 26; Indels 12; Gaps 8;
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OY	121	CAAGCTGGGATTTACAGGCATGTGCACACGCTGGCTAAATTTGATTTTTTTAG	180
Db	5566	TAGTAGCTGGGATTAACAGGCATGTGCACACGCTGGCTAAATTTGATTTTTTTAG	5507
OY	181	TAGAGATGAGAGTTTCCCATGTTGGTCAGGCGGTCTGAACTCCCGACCTCAGATGATC	240
Db	5506	TAGAGATGAGAGTTTCTCCATGTTGGTCAGGCGGTCTGAACTCCCGACCTCAGATGATC	5847
OY	241	CTTCGCTCTGGGCTCCCAAGTGCT--AGATACAGACATGGCCACATGCCCCG-CTC	256
Db	5846	CTCCGCTCTGGGCTCCCAAGTGCTGAGATTAACGGATGAGGCACATGCCCCGCTCC	5787
OY	297	TGCCGTGCTAAATTTTGTGGTGAAGAAACAGGGTTTCACTGATG-TGCCAACTGTGCTCC	355
Db	5786	TGCCGTGCTAAATTTTGTGGTGAAGAAACAGGGTTTCACTGATGTTGGCCAACTGTGCTCC	5727
OY	356	TGAGCTCAAGCAGTCCACCTGCTCAGCTCCCAAAAGTCTGGGATTAACAGCGT--GCA	413
Db	5726	TGAGCTCAACACGATCCACCTGCTCAGCTCCCAAAAGTCTGGGATTAACAGCGCTGAGCC	5667
OY	414	GGCTGGCTGGCCCTTTTATTTATTTTAAACACAGGTGCCACCTTAACCCAG	473
Db	5666	ACCGTGGCTGGCTTTTATTTATTTTAAACACAGGTGTGCCACTTAAACCAG	5607
OY	474	GATGAAGTGCAGTGTGTGATCATCAGCTCATGCGACCTTCAACTCTGAGATCAAGC-A	532
Db	5606	GATGAAGTGCAGTGTGTGATCATCAGCTCATGCGACCTTCAACTCTGAGATCAACGAA	5547
OY	533	TCCGCGCGCTCAGCCGCCAACGATGACTGGGACCAAAAGCATGACACATCACTGGCT	592
Db	5546	TCCGCGCGCTCAGCCGCCAACGATGACTGGGACCAAAAGCATGACACATCACTGGCT	5487
OY	593	AATTTTATTTTATTTTAAATTTTGAAGACAGATCTCACTGTCAACCCAGCGTG	652
Db	5486	AATTTTATTTTATTTTAAATTTTGAAGACAGATCTC-ACGTGACCCAGCGTG	5428
OY	653	AGTGCATGGCGCAATCTTGGCTCACTGCAACCTCTGCTCCCGGGTTCAGATTATCTC	712
Db	5427	AGTGCATGGCGCAATCTTGGCTCACTGCAACCTCTGCTCCCGGGTTCAGATTATCTC	5368
OY	713	CTGCGCCAGCCTCTGTAGTGTGGGACATACAGGCGCCACACGCCCTAGCTAAATTTTT	772
Db	5367	CTGCGCCAGCCTCTGTAGTGTGGGACATACAGGCGCCACACGCCCTAGCTAAATTTTT	5308
OY	773	TGTATTTTATAGTAGAGATGGGG--TTACACATGTTGGCCAGGGTATCTTGATCTGTGAC	831
Db	5307	TGTATTTTATAGTAGAGATGGGGTTTACACATGTTGGCCAGGGTGTCTTGATCTGTGAC	5248
OY	832	CTTGAGATGTGCCGCTCGGCGCTCCCAAAAGTCTGGGATTAACAGCGGAGACCCACG	891
Db	5247	CTTGATGTGCCGCTCGGCGCTCCCAAAAGTCTGGGATTAACAGCGGAGACCCACG	5188
OY	892	CCGGCTTATTTTAAATTTTGTGTGAAATGGAATCTCACTGTGTACACAGCGTG	951
Db	5187	CCGGCTTATTTTAAATTTTGTGTGAAATGGAATCTCACTGTGTACACAGCGTG	5128
OY	952	GAGTGCATGGCCAAATCTGGGCTGACCTGCAACCTGTGCTCCGGGGTCAAGCATCTT	1011
Db	5127	GAGTGCATGGCCAAATCTGGGCTGACCTGCAACCTTGTGCTCCGGGGTCAAGCATCTT	5068
OY	1012	CTGTCTCAGCCTCCCAAGCAGCTGGGATTAAGGGACCTGCAACACACCCCGCTAAT	1071
Db	5067	CTGTCTCAGCCTCCCAAGCAGCTGGGATTAAGGGACCTGCAACACACCCCGCTAAT	5010
OY	1072	TTTGTATTTTATTAAGAGGGGGTTTACACATTTTGTACAGGTGTCTCAACTCTG	1131
Db	5009	TTTGTATTTTATTAAGAGGGGGTTTACACATTTTGTACAGGTGTCTCAACTCTG	4950
OY	1133	ACCTCAGGTGACCACTGCTCAGCTTCCAAAGTGTGGGATTAACAGCGCTGAGCAC	1191
Db	4949	ACCTCAGGTGACCACTGCTCAGCTTCCAAAGTGTGGGATTAACAGCGCTGAGCAC	4890
OY	1192	CTCACCACGCGGCTAATTTAGATAAAAAATGTAGCAATGGGGGCTTTGTATGTT	1251

Db	4889	CTCACCCAGCCGGCTAAATTGATTAATAAATAATGTAGTACATGGGGGCTCTTGCTATGTT	4830
Qy	1252	GCCCAGCGTGGTCTCAACTCTGCTTCATGATCAATCCTTCCAAATGAGCCACAACCC	1311
Db	4829	GCCCAAGCTGGTCTCAACTCTGCTTCATGATCAATCCTTCCAAATGAGCCACAACCC	4770
Qy	1312	AGCCAGTCACATTTTAAACAGTTACATCTTTATTTAGTATACAGAAAGTAAATACAA	1371
Db	4769	AGCCAGTCACATTTTAAACAGTTACATCTTTATTTAGTATACAGAAAGTAAATACAA	4710
Qy	1372	TAAACATCTCAACCTGCAAATTCAGTGTGAACAGAGTCTTTTATATAACTTTTAAACAA	1431
Db	4709	TAAACATCTCAACCTGCAAATTCAGTGTGAACAGAGTCTTTTATATAACTTTTAAACAA	4650
Qy	1432	GCTTAG 1438	
Db	4649	GTATCAG 4643	

RESULT 6	AR051479	1381 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR051479				
DEFINITION	AR051479	Sequence 49 from patent US 5830670.			
ACCESSION	AR051479				
VERSION	AR051479.1	GI:5974843			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1381)				
TITLE	de la Monte,S. and Wands,J.R.				
JOURNAL	Neural thread protein gene expression and detection of Alzheimer's				
FEATURES	Patent: US 5830670-A 49 03-NOV-1998;				
source	Location/Qualifiers				
	1. 1381				
	/Organism="unknown"				
BASE COUNT	296 a 384 c 302 g 399 t				
ORIGIN					

Query Match	74.9%	Score 1080.2	DB 6	Length 1381
Best Local Similarity	94.4%	Pred. No. 0		
Matches 117	Conservative	0	Mismatches 53	Indels 25
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QY	2	TTTTTTTTTGAGATGAGATTTCGCTCTCTGTTGGCCAGGCTGAGTGCATGCGCAAT	61	
Db	1	TTTTTTTTTTGAGATGAGATTTCGCTCTCTGTTGGCCAGGCTGAGTGCATGCGCAAT	60	
QY	62	CTCAGCTACCCCAACCTCCGCGCTCCCGGGTTCAAGCAGATTCTCGCTCAGGCTCCGC	121	
Db	61	CTCAGCTACCCCAACCTCCGCGCTCCCGGGTTCAAGCAGATTCTCGCTCAGGCTCCGC	120	
QY	122	AGTAGCTGGAGATTACAGCGCATCTGCACCCAGCGCTGGGCTAAATTTTGTATTTTTTTAGT	181	
Db	121	AGTAGCTGGAGATTACAGCGCATCTGCACCCAGCGCTGGGCTAAATTTTGTATTTTTTTAGT	179	
QY	182	AGAGATGGAAGTT--CTCCATGTTGGTCAAGCTGGGTCTGGAAGCTCCGACCTCCAAATGAT	239	
Db	180	AGAGATGGAAGTTAAATCCATGTTGGTCAAGGCTGGGTCTGGAAGCTCCGACCTCCAAATGAT	239	
QY	240	CCCTCGCTCGGAGCTCCCAAAAGTGT--ACATACAGAGACAGGCGACCATCTCCGG--CT	295	
Db	240	CTCCGCTCTCGGAGCTCCCAAAAGTGTGAGATTACAGGCGATGAGCCACCATCTCCGGGCT	299	
QY	296	CTCGCCGAGCTAAATTTTGTGGTAGAAACAGGGTTTCACTGATG--TGCCCAAGCTGGTCTC	354	
Db	300	CTCGCCGAGCTAAATTTTGTGGTAGAAACAGGGTTTCACTGATGTTGCCCAAGCTGGTCTC	359	
QY	355	CTGAGCTCAAGAGTCCAGCTGCCTCAGGCTCCCAAGTGGTGGGATTTCAGGCGGAGC	414	
Db	360	CTGAGCTCAAGAGTCCAGCTGCCTCAGGCTCCCAAGTGGTGGGATTTCAGGCGGT--CAG	418	



OY	415	CGGTGGCTGAGCCTTTTATTTATTTATTTTAAACACACAGAGTGTCCTACTTTACCAGG	474
Db	419	CCGTGCCTGGCCTTTTTTAATTATTTTAAAAACACAGAGTGATGCCACTCTTACCACAG	478
OY	475	ATGAAGTCAGTAGTGATGATCACAGCTCACTGCAGCCCTTCAACTCCTAGATCAAGC-AT	533
Db	479	ATGAAGTCAGTAGTGATGATCACAGCTCACTGCAGCCCTTCAACTCCTAGATCAAGCAT	538
OY	534	-CCCTCGGCCACACCTCCCAAGTAGTGCGGGGACCAAAGCATGACACTACACTGGCTCA	593
Db	539	CCCTCGGCCACACCTCCCAAGTAGTGCGGGGACCAAAGCATGACACTACACTGG-7A	597
OY	594	ATTTTATTTTATTTTAAATTTTGTGAGACAGAGTCACACTGTCATCCAGGCTGGA	653
Db	598	ATTTTATTTTATTTTAAATTTTGTGAGACAGAGTCAC-ACTGTGTCACCAAGGCTGGA	656
OY	654	GAGCAATGGGCAATCTGGCTCACTGCACACCTGCTCCCGGGTTAAAGTATTTCTC	713
Db	657	GAGCAATGGGCAATCTGGCTCACTGCACACCTGCTCCCGGGTTCAAGTATTTCTCC	716
OY	714	TGCCCCAGCCTCCTGATAGTACTGGAGTACAGGCGCCACACAGCCCTGATTAATTTT	773
Db	717	TGCCCCAGCCTCCTGATAGTACTGGAGTACAGGCGCCACACAGCCCTAGTATTTT	776
OY	774	GATATTTTATAGTAGATGGGG-TTACCAATGTTCCGACAGTTGATCTTGATCTGACCC	832
Db	777	GATATTTTATAGTAGATGGGGTTACCAATGTTCCGACAGTTGATCTTGATCTTGACCC	836
OY	833	TGTGATCTGACCGCCTCGGCTC-CCCAAGTGCTGGAGTATACAGGCGCTGAGCACCA	891
Db	837	TGTGATCTGACCGCCTCGGCTCACCACCAAGTGCTGGAGTATACAG--GTGCTGACTCCAC	894
OY	892	CCCAGCTATTTTAAATTTTGTGTTGTTTAATGGAATCTCACTCTGTATACCAAGCTG	951
Db	895	GCCGCGCTATTTTAAATTTTGTGTTGTTTAATGGAATCTCACTCTGTATACCAAGCTG	954
OY	952	GAGTGCAATGAGCCAAATCTCGGCTCACTGCAACCTGSCCCTCCGGGCTCAAGGATCT	1011
Db	955	GAGTGCAATGAG-CAAAATCTCGGCTACTCGCAACCTGCTCCCGGG-TCAAGGATCT	1012
OY	1012	CCTGCTCAGCCTCCCAAGCAGTGGGATTAAGGGACCTGACACACACCCCGCTAAT	1071
Db	1013	CCTGCTCAGCCTCCCAAGCAGTGGGATTAAGGG--ACCTGCAACCAACCCCGCTAAT	1070
OY	1072	TTTGTATTTTCAATTAGAGCGGGGTTTACACATTTTGTAGAGCT-GATCTCAACACTCT	11330
Db	1071	TTTGTATTTTCAATTAGAGCGGGG--TTTACATATTTGTCAAGGCTGGGTCTCAAACTCT	1128
OY	1131	GACCTCAGGTGACCCACCTGCTCAGCCTTCCAAAGTGTCTGGGATTACAGCGGTGAGCCA	1190
Db	1129	GACCTCAGGTGACCCACCTGCTCAGCCTTCCAAAGTGTCTGGGATTACAGCGGTGAGCCA	1188
OY	1191	CCTCACCACGCGGGTAATTTAGATAAAAAAAATAATGAGCAATGAGGGGCTTCTCTATGT	1250
Db	1189	CCTCACCACGCGGGTAATTTGGATAAAAAAATATGAGCAATGAGGGG--TCTGTATGT	1246
OY	1251	TGCCAGGCTGGTCTCAAACTCTTGGCTTCATGCAATCTTCCAAATGAGCGACACAC	1310
Db	1247	TGCCAGGCTGGTCTCAAACTCTTGGCTTCATGCAATCTTCCAAATGAGCGACACAC	1306
OY	1311	CAGCAGTCACATTTTAAACAGTATACATCTTATTTTATGTAATACAGAAGTAATACA	1370
Db	1307	CAGCAGTCACATTTTAAACAGTATACATCTTATTTTATGTAATACAGAAGTAATACA	1366
OY	1371	ATAAACATGTCAAC 1385	
Db	1367	ATAAACATGTCAAC 1381	

RESULT 7					
AR072619					
LOCUS					
DEFINITION	AR072619	1381 bp	DNA	linear	PAT 28-AUG-2000
	Sequence 49	from patent	US 5948634.		

ACCESSION	AR072619
VERSION	AR072619.1
KEYWORDS	GI:99999383
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 1381)
TITLE	de la Monte,S., and Wands,J.R.
JOURNAL	Neural thread protein gene expression and detection of alzheimer's disease
FEATURES	Patent: US 5948634-A 49 07-SEP-1999;
source	Location/Qualifiers
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	/organism="unknown"
BASE COUNT	296 a 384 c 302 g 399 t
ORIGIN	

Query MatchScore	74.9%	Score	1080.2	DB	6	Length	1381
Best Local Similarity	94.4%	Pred.	No. 0				
Matches 1317; Conservative	0	Mismatches	53	Indels	25	Gaps	18

QY	2	TTTTTTTTTTAGAGTGGAGTTTCCCTCTTTGTGGCCACAGGCTGGAGTGAATGGGGCAAT	61
Db	1	TTTTTTTTTTAGAGTGGAGTTTCCCTCTTTGTGGCCACAGGCTGGAGTGAATGGGGCAAT	60
QY	62	CTCAGCTCACGCCAACCTCCGCCCTCCGGGTTCAAGCAATTCCTGCCTCAGCTCCCC	121
Db	61	CTCAGCTCACGCCAACCTCCGCCCTCCGGGTTCAAGCAATTCCTGCCTCAGCTCCCC	120
QY	122	AGTAGCTTGGGATTTACAGGCATGTGCACCCAGCCTGGCTAATTTTGTATTTTTTTTAACT	181
Db	121	AGTAGCTTGGGATTTACAGGCATGTGCACCCAGCCTGGCTAATTTTGTATTTTTTTTAACT	179
QY	182	AGAGATGGAGATTT--CTCCATGTTGGTAGGCTGGCTCGAAGCTCCGACCCAGATGAT	239
Db	180	AGAGATGGAGATTTAACTTCATGTTGGTAGGCTGGCTCGAAGCTCCGACCCAGATGAT	239
QY	240	CCCTCCGCTCTGGGCTCCCAAGTGCT--AGATACAGAGCTGGCCACCATGGCCGG-CT	295
Db	240	CTCCCGTCTCGGCCCTGCCCAAGTGCTGAGATTCAGGCATGAGCACCATGGCCGGCT	299
QY	296	CTGGCTGGCTAATTTTTTGTGTAGAAACAGGGTTTCACTGATG-TGCCAAGCTGGTCTC	354
Db	300	CTGGCTGGCTAATTTTTTGTGTAGAAACAGGGTTTCACTGATGTTGCCCAAGCTGGTCTC	359
QY	355	CTGAGCTCAACAGCTGCACCTGCCTCAGCTCCCAAGTGGTGGGATTTACAGGGCTGAG	414
Db	360	CTGAGCTCAACAGCTGCACCTGCCTCAGCTCCCAAGTGGTGGGATTTACAGGGCT-CAG	418
QY	415	CCGTGCTGGGCTTTTTAATTTTTTTTAAAGACACAGGTGTCGCCACTCTTACCCAGG	474
Db	419	CCGTGCTGGGCTTTTTAATTTTTTTTAAAGACACAGGTGTCGCCACTCTTACCCAGG	478
QY	475	ATGAAGTGCAGTGGTGTGTATCACAGCTACCTGCAGCCTTCAACTCTGTAGATTCAGC-AT	533
Db	479	ATGAAGTGCAGTGGTGTGTATCACAGCTACCTGCAGCCTTCAACTCTGTAGATTCAGC-AT	538
QY	534	CCCTCTGCCTCAGCTCCGCCAAGTAGCTGGGGCCAAAGACATGACACCTACACCTGGCTA	593
Db	539	CCCTCTGCCTCAGCTCCGCCAAGTAGCTGGGGCCAAAGACATGACACCTACACCTGG-TA	597
QY	594	ATTATTTATTTTAAATTTTAAATTTTAAAGACAGATGCATCTGTATCACCAGGCTGA	653
Db	598	ATTATTTATTTTAAATTTTAAATTTTAAAGACAGATGC-ACCTGTATCACCAGGCTGA	656
QY	654	GTCGAGTGGCGCAATCTTGGCTCAGTGCACCTCTGCGCTCCCGGGTTCAAGTTATTTCC	713
Db	657	GTCGAGTGGCGCAATCTTGGCTCAGTGCACCTCTGCGCTCCCGGGTTCAAGTTATTTCC	716
QY	714	TGGCCCGAGCTCTCGATAGCTGGGACTACAGAGGGCCACAGCGCTAAGTAAATTTTTTT	773
Db	717	TGGCCCGAGCTCTCGATAGCTGGGACTACAGAGGGCCACAGCGCTAAGTAAATTTTTTT	776

QY	774	GTATTTTCTAGTACGATGGG--TTACACCATGTTCCGACAGTTGATCTGTATCTCTGACC	832
Db	777	GTATTTTCTAGTACGATGGGTTTACACCATGTTCCGACAGTTGATCTGTATCTCTGACC	836
QY	833	TTTGATGATCGCTCCCTCCGCGCT--CCCAAGTGTGGGATTACAGCGGTAGCCACCACG	891
Db	837	TTTGATGATCGCTCCCTCCGCGCTACCAAGTGTGGGATTACAG--GTGGTACTCCAC	894
QY	892	CCCGGCTTATTTTAAATTTTGTGTTTGAATGAAATCTCACTCTGTTACCCAGCTG	951
Db	895	GCCGGCTTATTTTAAATTTTGTGTTTGAATGAAATCTCACTCTGTTACCCAGCTG	954
QY	952	GAGTGCATGAGCCAAATCTGGCTCAGTGCACCACTGTCCGCCCGGCGTCAAGGATTTCT	1011
Db	955	GAGTGCATGAG--CAATCTGGCTACTCTGCACACTCTGCTCCCGGG--TCAAGGATTTCT	1012
QY	1012	CCTGTCTCAGGCTCCCAAGCAGCTGGGATTACGGGCACTGCGCACACACCCGCTAATT	1071
Db	1013	CCTGTCTCAGGCTCCCAAGCAGCTGGGATTACGGG--ACCTGCACACACCCGCTAATT	1070
QY	1072	TTTGATTTTCAATAGAGCGGGGTTTACATTTTGTGAGGCT--GGTCCAAATCCT	1130
Db	1071	TTTGATTTTCAATAGAGCGGGG--TTTACATTTTGTGAGGCTGGGTCTCAACTCCT	1128
QY	1131	GACCTCAGGTGACCCACCTGCTCAGCCTTCCAAAGTCTGGGATTACAGGCGTAGACCA	1190
Db	1129	GACCTCAGGTGACCCACCTGCTCAGCCTTCCAAAGTCTGGGATTACAGGCGTAGACCA	1188
QY	1191	CCTCACCACCGCGCTAATTAGATAAAAAATATGTAGCAATGGGGGCTTCTCTATGT	1250
Db	1189	CCTCACCACCGCGCTAATTGGATTAATAAATATGTAGCAATGGGGG--TCTCTATGT	1246
QY	1251	TGCGCAGGCTGCTCAAACTCTGGCTTCATGCAATCCTTCCAAATGAGCCACACACC	1310
Db	1247	TGCGCAGGCTGCTCAAACTCTGGCTTCATGCAATCCTTCCAAATGAGCCACACACC	1306
QY	1311	CAGCCAGTCACTTTTAAACAGTTACATCTTTATTTAGTATACTGAAAGTAAATCA	1370
Db	1307	CAGCCAGTCACTTTTAAACAGTTACATCTTTATTTAGTATACTGAAAGTAAATCA	1366
QY	1371	ATTAACATGTCAAC	1385
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LOCUS	AR073164	1381 bp	DNA
DEFINITION	Sequence 49 from patent US 5948888.		Linear
ACCESSION	AR073164		
VERSION	AR073164.1	GI:9999927	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1381)		
TITLE	de la Monte,S. and Wands,J.R.		
	Neural thread protein gene expression and detection of Alzheimer's		
	disease		
JOURNAL	Patent: US 5948888-A 49 07-SEP-1999;		
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Best Local Similarity 94.4%; Pred. No. 0;			
Matches 1317; Conservative 0; Mismatches 53; Indels 25; Gaps 18;			
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OY	62	CTGAGCTACCCGACACCTCGCGCTCCCGGGTTCAAGGCATTTCTCTGCTCAGGCTCCCC	121
Db	61	CTCAGGCTACACGGACCTCGCGCTCCCGGGTTCAAGGCATTTCTCTGCTCAGGCTCCCC	120
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Db	121	AGTAGCTGGGATTACAGGCACTGTGCACCCAGCCTCGGCTAAATTTTGTATTTTTTTTAA	179
OY	182	AGAGATGGAGTTT--CTCAATGTTGTCTAGGCTGGTCTTCGAACCTCCGACCTGAGATGAT	239
Db	180	AGAGATGGAGTTTAACTCCATGTTGTGTCAAGGCTGGTCTTCGAACCTCCGACCTGAGATGAT	239
OY	240	CCCTCCGCTCAGGCTCCGCTCCCAAGTGT--AGATACAGAGCTCGGACCATGCCCAG--CT	295
Db	240	CTCCGCTCTCGGCTTCGCCAAAGTGTGTAGATTTACAGGATGAGGCACCATGCCCAGGCT	299
OY	296	CTGCGCTGCTAAATTTTGTGTAGAAACAGGGTTTCACTGATG--TGCCCAAGCTGTCTC	354
Db	300	CTGCGCTGCTAAATTTTGTGTAGAAACAGGGTTTCACTGATGTTGCCCAAGCTGTCTC	359
OY	335	CTGAGCTCAAGCACTCCAGCTCGGCTCAGGCTCCCAAGTGTGGGATTACAGGCGTGCAG	414
Db	360	CTGAGCTCAAGCACTCCAGCTCGGCTCAGGCTCCCAAGTGTGGGATTACAGGCGT--CAG	418
OY	415	CCGTGCGCTGGCTTTTATTTTATTTTAAAGACACAGGTGTCCCACTCTTACCCAGG	474
Db	419	CCGTGCGCTGGCTTTTATTTTATTTTAAAGACACAGGTGTCCCACTCTTACCCAGG	478
OY	475	ATGAAGTCACTGCTGTGTATCACAGCTCACTGACGCTTCAACTCTGTAGATCAAGC--AT	533
Db	479	ATGAAGTCACTGCTGTGTATCACAGCTCACTGACGCTTCAACTCTGTAGATCAAGCAT	538
OY	534	CCTCCTGCTCAGGCTCCCAAGTAGTGTGGGACCAAGACATCAGCACTACACCTGAGCTA	593
Db	539	CCTCCTGCTCAGGCTCCCAAGTAGTGTGGGACCAAGACATGACATGACATCACTACCTG--TA	597
OY	594	ATTTTATTTTATTTTAAATTTTGTGAGACAGATCTCACTGTCTACCCAGGCTGGA	653
Db	598	ATTTTATTTTATTTTAAATTTTGTGAGACAGATCTC--ACTCTGTCAACCAAGGCTGGA	656
OY	654	GTGCGATGGGCAATCTGTGGCTACGTCAACCTGTGCTCCCGGGTTCAGTTATTTCC	713
Db	657	GTGCGATGGGCAATCTGTGGCTACGTCAACCTGTGCTCCCGGGTTCAGTTATTTCC	716
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Db	717	TGCCCCAGCCTCTGAGTAGCTGGGACTACAGGCGCCACACGCTCACTAATTTTTT	776
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Db	777	GTATTTTATTTAGTAGATGGGGTTTCCACATGTTCCGAGGTGATCTGATCTCTTGAC	836
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OY	1251	TGCCCAGGGTGGTCTCAAACTCTGGCTCATGCAATCCTTCCAAATGAGCCACAACACC	1310
Db	1247	TGCCCAGGGTGGTCTCAAACTCTGGCTCATGCAATCCTTCCAAATGAGCCACAACACC	1306
OY	1311	CAGCCAGTCACATTTTAAACAGTTACATCTTTATTTAGTATACTAACAAGTAATTACA	1370
Db	1307	CAGCCAGTCACATTTTAAACAGTTACATCTTTATTTAGTATACTAACAAGTAATTACA	1366
OY	1371	ATAAACATGTCAAAC	1385
Db	1367	ATAAACATGTCAAAC	1381

RESULT	9
LOCUS	AC087434
DEFINITION	AC087434 160714 bp DNA linear HTG 05-JAN-2001 Pan troglodytes clone RP43-90F9, WORKING DRAFT SEQUENCE, 12 unordered pieces.
ACCESSION	AC087434
VERSION	AC087434.1 GI:12039251
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT. Pan troglodytes.
SOURCE	Pan troglodytes
ORGANISM	Pan troglodytes

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 160714)	Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Ho, S.-L., Idol, J.R., Karlins, E., Lee-Lin, S.-Q., Legaspi, R., Lim, M., Maduro, Q. L., Maduro, V.B., Mastello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y., Snyder, B., Stantitrop, S., Thomas, J.W., Thomas, P.J., Tjongsom, E.E., Touchman, J.W., Tsirgson, C., Vogt, J.L., Walker, M.A., Wehber, K.D., Zhang, L.-H. and Green, E.D.	NISC Comparative Sequencing Initiative		
2 (bases 1 to 160714)	Green, E.D.	Unpublished		
		Direct Submission		
		Submitted (05-JAN-2001)		
		Grovmont Circle, Gaithersburg, MD 20877, USA		
		Genome Center		
		Center: NIH Intramural Sequencing Center		
		Web site: <a href="http://www.nisc.nih.gov">http://www.nisc.nih.gov</a>		
		Contact: nisc-mouse@hgri.nih.gov		
		Project Information		
		Center project name: ad		
		Center clone name: 090F09		
		Summary Statistics		
		Sequencing vector: plasmid; n/a; 100% of reads		
		Chemistry: Dye-terminator Big Dye; 100% of reads		
		Assembly program: Phrap; version 0.990319		
		Consensus quality: 152563 bases at least Q40		
		Consensus quality: 154387 bases at least Q30		
		Consensus quality: 155752 bases at least Q20		
		Insert size: 137000; agarose-fp		
		Insert size: 137000; pulse-field-gel		
		Insert size: 159614; sum-of-ctrls		
		Quality coverage: 9.32x in Q20 bases; agarose-fp		
		Quality coverage: 9.32x in Q20 bases; pulse-field-gel		
		Quality coverage: 8.00x in Q20 bases; sum-of-ctrls		
		NOTE: This is a 'working draft' sequence. It currently		
		* consists of 12 contigs. The true order of the pieces		

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* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
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* 2808: contig of 2808 bp in length
* 2809
* 2908: gap of unknown length
* 2909
* 6190: contig of 3282 bp in length
* 6191
* 6290: gap of unknown length
* 6291
* 12538: contig of 6248 bp in length
* 12539
* 12538: gap of unknown length
* 12839
* 20815: contig of 8177 bp in length
* 20816
* 20915: gap of unknown length
* 28981: contig of 8066 bp in length
* 28982
* 29081: gap of unknown length
* 29082
* 40689: contig of 11618 bp in length
* 40700
* 40799: gap of unknown length
* 49520: contig of 8721 bp in length
* 49521
* 49620: gap of unknown length
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* 62547: contig of 12927 bp in length
* 62548
* 62647: gap of unknown length
* 62648
* 76465: contig of 13618 bp in length
* 76466
* 76565: gap of unknown length
* 98277: contig of 21112 bp in length
* 98278
* 98377: gap of unknown length
* 127174: contig of 28797 bp in length
* 127274
* 127275: gap of unknown length
* 127275
* 160714: contig of 33440 bp in length.
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* Location/Qualifiers
FEATURES

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Dh 132680	TAGCTGGGATTCACAGGATGTGTCCACACACCTGGCTAATTTTTTGTATTTT	132735
Oy 184	AGATGGAATTTCTCCATGTTGGTGCAGAGCTGTCTCGAATCTCCGAGCTCAGATGATCCCT	243
Dh 132736	AGACGGGGTTTCTCATGTGTGTGAGTTGGTCTTGAACCCCGACCTCAGATGATCCG	132795
Oy 244	CCGCTCGGCTCCCAAGTGCATGATACAGGACTGTGCACCATGCCCGGCTCGCCCTGG	303
Dh 132796	CCACTTGGCTCCCAAGTGCATGATACAGGACTGTGTGCACCATGCCCGGCTCGCCCTGG	132854
Oy 304	CTAATTTTTGTGTAGAAACAGGCTTTCAGTGTGCCCAAGCTGGTCTCTGAGCTCA	363
Dh 132855	AGTATGAAGAGATACCTCCGGATATGGCGGGCCCTCCAAACCCACTTTGAAGATC	132914
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Oy 420	-----CGGGCTTTTATTTTATTTTATTTTAAACAGAGGTGTCCACCTTGA	468
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Oy 469	CCGAGATGAAGTGCAGTGTGTATACAGCTACAGCTCAGCACTCAACTGTGATTC-	527
Dh 133034	CCGAGCTGGAGTGCAGTGTGTATACAGCTACAGCTCAGCACTCAACTGTGATTC	133093
Oy 528	AAGCATCTCTGCTCAGCTCCCAAGTACGTGGAGCCAAAGACATGACACACTACAC	587
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Dh 133392	CTGAGCTGAGAGATCTCTGCTCGGCTCCCAAGGCTGGGATTTACAGGGGTGAG	133451
Oy 885	CACCAAGCCCGG-CTTATTTTATTTTATTTTATTTTATTTTGAATGGAATCTCACTGT	943
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Dh 133572	GGGATTTCTGCTCAGCTCAGCTCCCAAGAGGTAGGACTACAGGATGTGCTCCACAC	133631
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Dh 133632	GGCTAATTTTGTATTTTATTTTATTTTATTTTATTTTATTTTGAAGGCTGTGCT	133691
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Db 133692	AACGCTCAACTTCAGGTGATCCACCCCGCCCTGCGCTCCCAAGTGTGGATTACAGGCA	133751
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RESULT	10
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LOCUS	
DEFINITION	99370 bp DNA, linear PRI 30-SEP-2006
ACCESION	ACCO05057 Homo sapiens BAC clone CTB-52h6 from 7q11.2-q22, complete sequence.
VERSION	ACCO05057.2 GI:6587915
KEYWORDS	HTG.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens

REFERENCE  
1 (bases 1 to 99370)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE	AUTHORS	TITLE	JOURNAL
1	(bases 1 to 99370)	Sulston, J.E. and Waterston, R.	Toward a complete human genome sequence
Genome Res.	8 (11), 1097-1108		(1998)

MEDLINE	99063792
PUBMED	9847074
REFERENCE	2 (bases 1 to 99370)

AUTHORS	Dauphin, S., Stoneking, T. and Ahrens, C.
TITLE	The sequence of Homo sapiens BAC clone CTB-52H6
JOURNAL	Unpublished

REFERENCE	3 (Dases 1 to 993/0)
AUTHORS	Waterston, R.H.
TITLE	Direct Submission

JOURNAL  
Submitted (12-JUN-1998) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
0007-1226/98/0000-0000\$05.00/0

REFERENCE	4 (bases 1 to 993/0)	
AUTHORS	Waterston, R.H.	
TITLE	Direct Submission	
FORMATTED	Submitted (1000)	Genome Sequencing Center
FORNARD		Washington

JOURNAL  
SUBMITTED (16-Dec-1997) GENOME  
UNIVERSITY SCHOOL OF MEDICINE, 4444 FOREST PARK PARKWAY, ST. LOUIS,  
MO 63108, USA  
E (Baker) 140.00370)

REFERENCE	AUTHORS	TITLE	Journal	Department of Genetics	Washington
3 (cases 1 to 3330)	Waterston, R.	Direct Submission	Submitted (30-sep-2000)		

DOCUMENT# D0681176  
DATE RECEIVED 09 Dec 2006  
DEPARTMENT OF AGRICULTURE  
UNIVERSITY, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
On Dec 16, 1999 this sequence version replaced gi:3212934.  
----- Genome Center -----

Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu/wgsc>

-----  
 Contact: sapience@watson.wustl.edu  
 -----  
 Summary Statistics  
 -----  
 Center project name: H RG052H06

NOTICE: This sequence may not represent the entire insert of this

clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate

chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence

from more than one subclone; and the assembly was confirmed by restriction digest.

**MAPPING INFORMATION:**  
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.mrgi.nih.gov/DIR/CTB/CHR/>, send mailto:egreen@mrgi.nih.gov, or see <http://genome.wustl.edu/gsc>

**SOURCE INFORMATION:**  
Clone CTB-52H6 is from the first release of the human BAC library CTB-978SK-B. The library contains cloned DNA from the male fibroblast cell line 978SK. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-U. Kim et al., Genomics 34:213-8 (1996). This clone is available from Research Genetics, Inc. (<http://www.resgen.com>).  
VECTOR: pBeloBAC11  
Selection: chloramphenicol

**NEIGHBORING SEQUENCE INFORMATION:**

The clone sequenced to the left is CTA-270D13. Actual start of this clone is at base position 135330 of CTA-270D13; actual end is at base position 99370 of CTB-52H6.

**Location/Qualifiers****FEATURES**  
**source**

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LOCUS AX335496  
DEFINITION Sequence 6005 from Patent W00194629.  
ACCESSION AX335496  
VERSION AX335496.1 GI:18126215  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,  
Horlidan,S., Soppet,D.R. and Weaver,Z.  
TITLE Cancer gene determination and therapeutic screening using signature  
gene sets  
JOURNAL Patent: WO 0194629-A 6005 13-DEC-2001;  
Avalon Pharmaceuticals (US)  
FEATURES  
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DEFINITION Human LIM-kinasel and alternatively spliced LIM-kinasel (LIMK1)
gene complete cds.
ACCESSION U62293
VERSION U62293.1 GI:1432163
KEYWORDS Williams syndrome.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
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AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
Franziska J., J.M., Ewart, A.K., Morris, C.A., Mervin, C.B.,
Bertand, J., Robinson, B.F., Klein, B.P., Ensing, G.J., Everett, L.A.,
Green, E.D., Proschel, C., Gutowski, N.J., Noble, M., Atkinson, D.L.,
Odelberg, S.J., and Keating, M.T.
LIM-kinasel hemizyosity implicated in impaired visuospatial
constructive cognition
Cell 86 (1), 59-69 (1996)
JOURNAL MEDLINE 8689688
PUBMED 96291399
TITLE 2 (bases 1 to 65608)
AUTHORS Franziska J., J.M., Odelberg, S.J., Atkinson, D.L., and Keating, M.T.
JOURNAL Direct Submission
TITLE Submitted (25-JUN-1996) Human Genetics, Univ. of Utah, 10 N 2030 E,
Bldg 533, Suite 2100, Salt Lake City, UT 84112, USA
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KEYWORDS	Williams syndrome.					
SOURCE	Homo sapiens.					
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AUTHORS	1 (bases 1 to 67046) Osborne,L.R., Martindale,D.W., Scherer,S.W., Shi,X.-M., Huizenga,J., Heng,H.-H.Q., Costa,T., Pober,B., Lew,L., Brinkman,J., Rommens,J., Koop,B.F. and Tsui,L.-C.					
TITLE	Identification of genes from a 500-kb region at 7q11.23 that is commonly deleted in Williams syndrome patients					
JOURNAL	Genomics 36 (2), 328-336 (1996)					
MEDLINE	96411691					
PUBMED	8812460					
REFERENCE	2 (bases 1 to 67046) Martindale,D.W., Wilson,M.D., Wang,D., Burke,R.D., Chen,X., Duronio,V. and Koop,B.F.					
AUTHORS	Comparative genomic sequence analysis of the Williams syndrome region (LIMK1-RFC2) of human chromosome 7q11.23					
TITLE	Mamm. Genome 11 (10), 890-898 (2000)					
JOURNAL	20458868					
MEDLINE	11003705					
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REFERENCE	Direct Submission					
AUTHORS	Submitted (12-Jul-1996) Biology, University of Victoria, PO Box 1700, Victoria, BC V8W 2Y2, Canada					
TITLE	4 (bases 1 to 67046) Martindale,D.W., Osborne,L.R., Scherer,S.W., Tsui,L.-C. and Koop,B.F.					
JOURNAL	Human genomic sequence containing the complete LIM-kinase gene (LIMK1) and the 3' end of elastin (ELN)					
MEDLINE	Unpublished					
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Qy	637	CTGTACACCAGGCTGGAGATGCAAGGCGCAATCTGTGCTCACTGCAACCTGTGCTCCCG	696
Db	1216	CTGTCA-CCAGGCTGGAGATGCAAGTGGCTGTACTTGGCTCACTGCAACCTCGCTCCCG	1274
Qy	697	GATTCAAATTAATTCCTCTGCCCCAGCCCTCTAGTAGCTGGGACTACAGGCGCCACAC	756
Db	1275	GATTCACGCCAATTCCTCTG-CCGACCTCTCTCAAGTAGCTGGGACTACAGGCGCCGCGAC	1333
Qy	757	GCCTAGCTAAT-TTTTTTGTATTTTAAAGATGGGG-TTCACCATGTTGCCAGTT	814
Db	1334	CATGCCCGGCTAATTTTGTATTTTAAAGAGGGGGTTTCACCATGTTGCCAGGAT	1393
Qy	815	GATCTGTGATCTGTGAGCTTGATGATCTGCTGCCCTCCGCGCCCAAGCGTGGGATTAAC	874
Db	1394	GATCTCAAACTCTGTACTCATGATTCACCCACCTCAGCCTCCCAACTGCTGGGATTAAC	1453
Qy	875	AGGCGTGAAGCCACCAAGCCCGGCTTATTTTAAATTTTGTGTTTGAATGGAATCTCA	934
Db	1454	AGGTGTGAGCCATCAGCGCCAGCCCTTTTTTTTTTTTTT-----TAGATCTAAC	1504
Qy	935	CTCTGTTCACCAAGCTGGAGTGCATATGGCCAAATCTCGGCTCATCTGCACCTCTGCTCC	994
Db	1505	CTCTGTGGCCAGGAGGAGTGCACATGTGCGTGTATTGGCTACATGCAAAACCGCCCTCC	1564
Qy	995	CGGCGTCAAGGATCTCCTGTCTCAGGCTCCCAAGCAGCT	1035
Db	1565	CGGTTCAAGCAATTCCTCTGCTTAGTCTCCGAGTGTCT	1605

RESULT 3						
A0739838/C						
LOCUS	A0739838	877 bp	DNA	linear	GSS	16-JUL-1999
DEFINITION	H5_5J05_A1-CO9-T7A RPT-11 Human Male BAC Library Homo sapiens genomic clone Plate=1081 Col=17 Row=E, DNA sequence.					
ACCESSION	A0739838					
VERSION	A0739838.1	GI:5517260				
KEYWORDS	GSS,					
SOURCE	human.					
ORGANISM	Homo sapiens					
	Eumetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
REFERENCE	1 (bases 1 to 877)					
AUTHORS	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.					
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome					
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	96 (17),	9739-9744	(1999)		
MEDLINE	99380589					
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center					

	<p>University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@es.jong.med.buffalo.edu). Clones may be purchased from BACPacResources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu</p> <p>Plate: 1081 Row: E Column: 17 Seq primer: T7 Class: BAC ends</p> <p>High quality sequence stop: 877.</p>						
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	/clone="plate=1081 Col=17 Row=E"						
	/clone_id="RPCI-11 Human Male BAC Library"						
	/sex="male"						
	/note="Vector: pBACe3.6; Site.1: EcoRI; Site.2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"						
BASE COUNT	251 a 181 c 242 g 203 t						
ORIGIN							
Query Match	27.1%; Score 391.4; DB 17; Length 877;						
Best Local Similarity	79.4%; Freq. No. 1.5e-62;						
Matches 514; Conservative 0;	Mismatches 126; Indels 7; Gaps 4;						
OY	568	AAGACATGCACACACATACACCTGGCTAAATTTTATTATTATTTTATTTTGAGACAGA	627				
DB	680	AACACTCCGCCAGTAATGATGTCTTTTTGTTATTGTTGTTTTTTGAGACAGA	621				
OY	628	GTCACAATCTGTGTCAOCCAGSGCTGAGTAGTCAGTGGCGCATTTGGCTACTGTCAACC	687				
DB	620	GTCCT-ACCTTTGATCCCCCAGGCTGGAGTACAGTGTGCATCTCAGCTCACGCAACCT	562				
OY	688	TGCCCTCCGGGGTTCAAGTAATCTCCTGGCCCAGGCTCCTGATAGCTGGACTACAGGC	747				
DB	561	CGCCTGCCAGGTTCAAGCAATTCCTGCTAGGCTCCCACTAGCTGGAATAAGGT	502				
OY	748	GC--GCACACAGCCTAGCTAATTTTTTTGTAATTTTATAGATAGATGGGGTTCCACANT	804				
DB	501	GCGTCGACACAGCCACAGCTAATTTTATTTTATTTAGTAGACACA-GGGTTTCACCATGT	443				
OY	805	TGCGCAGGTGATCTTGATCTCTGGACCT-TGTATCTGCCTGGCTGGGCTCCCAAG	862				
DB	442	TGGCCAGGGCTTCTTTGAACCTCTGACCTCAAGCAAGCAATCGGTAGGCTTGGCTCCCAAAG	383				
OY	863	TGCTGGATTAAGAGCGTAGGCAACACAGCCCGGCTATTTTAAATTTTGTGTTTGA	922				
DB	382	TGCTGGATTAAGAGGTAGCGCACCGACCCACCAACCAAGTAATTTTTTTTTTTTTTGA	323				
OY	923	AATGATCTCACTCTGTTAACCCAGGCTGGAGTGCATGAGTGGCCAATCTGGCTCACTGA	982				
DB	322	GATGGATCTCACTCTGTTAACCCAGGCTGGAGTGCATGAGTGGCCAATCTGGCTCACTGA	263				
OY	983	ACCTGACCTCCCGGGCTGAAGGATTCCTGCTGACAGCTCCCAAGCAGCTGGGATTA	1042				
DB	262	ACCTGACCTCCCGAGTTAAGGATTCCTGCTGACAGCTCCCAAGCAGTGGGAAATA	203				
OY	1043	CGGGCAGCTGCACACACACCCGCTAATTTTGTATTTTCAATTAGAGCGGGGTTTCAAC	1102				
DB	202	CGGGCAGCTGCACACATGCCCGGCTAATTTTGTATTTTATAGAGACAGGGGTTTCGCC	143				
OY	1103	ATAATTGTAGGCTGGTTCAAATCTGACCTGACAGTACCACCTGGCTCAGGCTTCC	1162				
DB	142	ATGTTGTCAGAGGTTTCTTCGAACTCTCACTCAGTATATGCTTACTTCAAGCTCC	83				

OY	1163	AAAGTCGTGGGATTTACAGCCGCAGCACCACTTACAGCGCCTTAAT	1209
Dd	82	AAAGTCGTGGGATTTTAGCATGAGCCACCACACATCTGCCACAGTAAT	36
RESULT 4			
AUT762220/c			
LOCUS	AV762220	MDS Homo sapiens cDNA clone MDCB07 5'	mRNA linear EST 19-OCT-2000
DEFINITION	AV762220		
ACCESSION	AV762220.1	GI:10920068	
VERSION			
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Carnathrin; Homnidae; Homo.		
TITLE	1 (bases 1 to 1345)		
JOURNAL	Gu,J., Zhao,M., Huang,Q., Xu,X., Li,Y., Peng,Y., Song,H., Xiao,H., Gu,Y., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu.Z., Zeng, L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu.G., Yang Y., Gao.G., Zhang.Q., Chen.S., Han.Z. and Chen,z. Homo sapiens cDNA MDS clones Unpublished (2000) Contact: Zeguang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex.45) Fax: 86-21-50801922 Email: hanzg@chgc.sh.cn This clone is available at CHGC in Shanghai. Location/Qualifiers 1..1345 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="MDCB07" /clone_id="MDS" /tissue_type="Bone marrow" /cell_type="CD34+ hematopoietic stem/progenitor cell" /lab_host="BM25_8" /note="Vector: pTRIPlex2; Site_1: sfIIV; site_2: sfilIB"		
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Best Local Similarity	82.8%;	Pred. No. 3.5e-61;	
Matches 502;	Conservative 0;	Mismatches 86;	Indels 18; Gaps 5;
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Dd	606	ATTTTNTNNTTTTTTTTTTGTAGAAGCAGTCTC-ACTGTGCGCCACAGCTGAAGTGCAG	548
OY	660	TGGGCAATCTTGCTCACTGCAACTCTGCTCCCGGTTCAAGTAAVCTCTGCCCCC	719
Dd	547	TGGGATGATCTCACTGCTCAACTCTGCTCCCGGTTCAAGCAATCTCTGCTC	488
OY	720	AGCTCTCGATACTGGAGTACAGGCGC---CCACGAGCCCTAGCTAATTTTTTTGTA	776
Dd	487	AGCTCTCGATACTGGAGTACAGGCGCGCTCCACACCCACAGCTAAATTTTTGTATT	428
OY	777	TTTTTAGTAGAGAGGGGTCACCATGTCGSCAGAGTTGATCTGATCTGTGAGCTTGT	836
Dd	427	TTTAGTAGAGAGCA-GGGTTTCATCATGTGGCCAGCGCTTGCTTGAACCTCTGACCTGT	369
OY	837	GATCTGCCCTGCGCCGCCCAAGTGTGGATACAGGCGTGAGGACACACACCGCGG	896
Dd	368	GATCTGCCCTGCGCCGCCCAAGTGTGGATACAGGCGTGAGGACACACCGCGG	309
OY	897	C-----TTAATTTTAAATTTTGTGTGTGAATGAAATTCACATCTGTACCC	945
Dd	308	CTCATTTTGCATCTCTTTTTTTTTTTTTTTTTTTTTTTTGAGATGAGATCTCATCTAATTGCG	249

QY	946	AGCGTGAAGTGC	AAATGCGCAAAATCTGGCTCACTGCACCTTGCCCTCCGGAGCTCAAGC	1005
Db	248	AGCGTGAAGTGC <td>CTGTGGCAACATCTGGCTCACTGCACCTTGCCCTCCGGAGTTAAAGT</td> <td>189</td>	CTGTGGCAACATCTGGCTCACTGCACCTTGCCCTCCGGAGTTAAAGT	189
QY	1006	GATTCCTCTGTCT <td>CACGCTCCCAAGCAGCTGGGATTTACGGGACACCTGCACACACCCCG</td> <td>1065</td>	CACGCTCCCAAGCAGCTGGGATTTACGGGACACCTGCACACACCCCG	1065
Db	188	GATTCCTCTGTCT <td>CAAGCTCCCGCTCCCGCTCCCGAGTAGCTGGATTTACAGCATGACACCATGCTCCAG</td> <td>129</td>	CAAGCTCCCGCTCCCGCTCCCGAGTAGCTGGATTTACAGCATGACACCATGCTCCAG	129
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QY	1126	CTCCGTACCTCAGGT <td>AGACCCACCTGCTCAGCCTTCCAAAGTCTGGATTTACAGGCTGTG</td> <td>1185</td>	AGACCCACCTGCTCAGCCTTCCAAAGTCTGGATTTACAGGCTGTG	1185
Db	68	CTCCGTACCTC--	GGATTCGCGCCCGGCTCAGCCTCCCAAAAGTCTGGATTTACAGGCTGTG	11
QY	1186	AGCCAC	1191	
Db	10	AACCAC	5	
RESULT 5				
LOCUS	BQ722917	910 bp	mRNA	linear
DEFINITION	AGENCOURT_8100507	lupski_sympathetic-trunk	Homo sapiens	CDNA clone
ACCESSION	IMAGE:6190443	5'	mRNA sequence.	
VERSION	BQ722917			
KEYWORDS	BQ722917.1	GI:21861803		
SOURCE	EST.			
ORGANISM	human.			
REFERENCE	Homo sapiens			
AUTHORS	Enkaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;			
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
JOURNAL	1 (bases 1 to 910)			
COMMENT	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Dr. James R. Lupski CDNA Library Preparation: Life Technologies, Inc. DNA sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LAM13589 row: e column: 04 High quality sequence stop: 653. Location/Qualifiers 1..910 /organism="Homo sapiens" /db_xref="taxon:9606" /clone IMAGE:6190443" /clone_id="lupski_sympathetic-trunk" /sex="male" /tissue_type="sympathetic trunk" /dev_stage="adult, 16 yr" /lab_host="DH10B" /note="vector: pCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. directionally cloned using the following adaptors: 5'-GACATCCACGATCGCG-3' and 5'-GACATGTCGATCGGAGCGGCCGCT(15)-3'. Size selected > 1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies.."			
FEATURES				
source				
BASE COUNT	277 a	224 c	268 g	140 t
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Query Match	26.3%	Score 379:	DB 14:	Length 910:
Best Local Similarity	80.8%	Pred. No. 2.8e-60:		





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/clone="IMAGE:6104226"
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/notes="Organ: testis; Vector: pDNR-lin (Clontech); Site.1:
sfiI (ggccgcctcgcc); Site.2: SfiI (ggccatcattggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCCATTTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAAGAGCGCCAGCGCGCCGACATC-drr(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."

```

CUNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)





QY 1021 GCCTCCAGACAGCTGGATTACGGACCTGCCACACACCCGCTAATTTTGTATT 1080  
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Db 3562 GCCTCCAGACAGCTGGATTACGGACCTGCCACACACCCGCTAATTTTGTATT 3617  
QY 1081 TCATTAGAGCGGGTTTACCATTTTGTACAGCTGCTCAAACTCTGACCTCAGGT 1140  
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Db 3618 TAGTGAATAGGGTTTACCATTTTGTACAGCTGCTCAAACTCTGACCTCAGGT 3677  
QY 1141 GACCCAGCTGCTCAGCTTCCAAAGTGGGATTACAGGCTGACGACCTACCTACCCAG 1200  
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Db 3678 GATCCAGCTGCTCAGCTTCCAAAGTGGGATTACAGGCTGACGACCTACCTACCCAG 3737  
QY 1201 CC 1202  
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Db 3738 CC 3739  
RESULT 12  
LOCUS BC024593 4087 bp mRNA linear HTC 07-AUG-2002  
DEFINITION Homo sapiens, clone IMAGE:3914314, mRNA.  
ACCESSION BC024593  
VERSION BC024593.1 GI:22137609  
KEYWORDS HTC.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 4087)  
AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (01-MAR-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-rt@mail.nih.gov](mailto:cgapbs-rt@mail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>  
Contact: (Dickson, Mark) [md@paxil.stanford.edu](mailto:md@paxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
R. M.  
Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>  
Series: IRAK Plate: 22 Row: m Column: 14  
This clone was selected for full length sequencing because it  
passed the following selection criteria: Hexamer frequency ORF  
analysis  
This clone has the following problem: Incomplete processing.  
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Db 1309 TTTTATTTTATGATGAGTCTT--GCCCTGTACCCAGAGCTGAGTGCAGTGGCGCA 1366  
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QY 347 -----CTGCTCTCTGAGCTCAAGCAGTCCAGCTGCTCAGCTCC 388  
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QY 389 AAATGCTGGGATTACAGGCTGTGACGCTGCTGCTGCTTTTATTTTATTTTAA 448  
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Db 1723 GTGTAGCTGGGATTATAGCATGACAC--ACCATCTCGGCTAATTTTATTTAGTGA 1779  
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Db 1780 GACAGGCTGTGCTATGTTGCTGACAGCTGTCT--CAACTCTGACCTGAGCAGCAGCAG 1838  
QY 509 GCCTTCACTCTGAGATCAAGCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 568  
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QY 767 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 825  
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QY	991	CTCCCGGCGCTCAGCATTCTCTCTCAGCTCCCAAGCAGTGGGATTACGGGACC	10950
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QY	1051	TGCCACACCAACCCCGCGTAATTTTGTATTTTCATTAGAGGCGGGGTTTCACCATATTGT	1110
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DEFINITION	AV700988	GRC Homo sapiens cDNA clone GKCAE01.3,	mRNA sequence.
ACCESSION	AV700988		
VERSION	AV700988.1	GI:10302959	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.		
AUTHORS	1 (bases 1 to 839)		
	Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yao,Q., Cai,T., Zhang,X., Xiao,H., Qian,J., Lu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Hu,G., Gu,J., Chen,Z., and Han,Z.		
	Shen,K., Lu,G., Fu,G., Zhong,W., Xu,S., Gu,W., Huang,W., Zhao,X.,		
	Insight into hepatocellular carcinogenesis at transcriptome level		
	by comparing gene expression profiles of hepatocellular carcinoma		
	with those of corresponding noncancerous liver		
	Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)		
JOURNAL	21625106		
COMMENT	Contact: Zeguang Han		
	Chinese National Human Genome Center at Shanghai		
	351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai		
	201203, P. R. China		
	Tel: 86-21-50801919(ex.45)		
	Fax: 86-21-50801922		
	Email: hanzg@hgc.sh.cn		
	This clone is available at CHGC in Shanghai.		
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Best Local Similarity	81.4%;	Pred. No. 5.5e-58;	
Matches 499; Conservative	0;	Mismatches 101;	Indels 13; Gaps 6;
QY	602	TTTTATTTTAAATTTTGGAGACAGAGTCTCAACTCTGTCCACCAGGCTGAGTGAAGTG	661
Db	66	TTTATTTTATTTTATTTTGGAGCAGAGTCTGAGTGTGTCACCCAGGCTGAGTGAAGTG	124
QY	662	GGCGAATCTTGGCTCACTGCAAACTCTGCTCCGCGGTTCAAGTTATTCTCTGCCCCAG	721
Db	125	GGCGAATCTTGGCTCACTGCAAACTCTCTCCGCGGTTCAACCCCAATTCCTCTCCCTCAA	184

FEATURES	Location/Qualifiers
Db	1196 CCCAGCCGCGTAA 1208
Db	659 CCTGGCCGCAAA 671
Db	1136 CAGGAGACCACCTGCTGAGCTTCCAAAGTGTGGATTAACAGGCGTAGAGCCACTCA 1195
Db	599 CAGGAGAACCGCCACACTTAGTACGCTCCCAAGTGTCTGGATTACAGGCGTAGAGCCACTCA 658
Db	539 TATTTTATAGCAAGATGGGGGTTTATACATGCTGGCCAGGCTGTCTTGAACCTCTACAT 598
Db	1076 TATTTTATAGCAAGCGGGGTTTACACATATTTGTAGAGCTGGTCTCAAACTCCTACCT 1135
Db	479 TCAGCGCTTCCAAATGAGTCTGGGATTCAGAGTGGCCACACAGCGCTGACTATTTTGG 538
Db	1018 TCAGCC-TCGCAAGCAGCTGGGATTAACGGGCACTGGCCACACACACCCCGCTA-ATTTTGG 1075
Db	419 AGTGAAGCATCTCGGCTCAGTCAACCTCCGCTGCTGGTTCAAGATTCCTCTGCC 478
Db	958 AATGGCAATCTCGGCTCAGTCAACCTCTGCTCCGAGGCTCAAGCAATCTCCTGTC 1017
Db	365 CACT-----TATTTTATTTTGTGAATGATGATCTACACTGCTACCTGCGGGAGTGC 418
Db	898 TTAATTTTATTTTGTGTGTTGTTGAATGGAATTCACCTCTGTTACCAGGGCGGGAGTGC 957
Db	305 ATCTGCTGCTCCGCGCTCCCAAAGTGTGGGATTCAGAGCTTGAGCCACCGCACCCGCG 364
Db	838 ATCTGCTGCTCCGCGCTCCCAAAGTGTGGGATTCAGAGCTTGAGCCACCGCACCCGCG 897
Db	245 TTTTATAGAGAGCGGGTTTACCGCTTATAGCAGATGCTGTGATCTCTGACCTGTG 304
Db	779 TTTTATAGAGAGGGG-TTCACCATGTTGCGCAGGTTGATGTTGATCTCTGACCTGTG 837
Db	185 CTTCCCGATACCTGTGATTAACAGGGGTTGCGCACACCGCCGACTAATTTTGTATTT 244
Db	722 CCTCTGATGACTGGGACTACAGGG---CCACACGCGCTAGCAATTTTGTATTT 778
Db	1196 CCCAGCCGCGTAA 1208
Db	659 CCTGGCCGCAAA 671
Db	1136 CAGGAGACCACCTGCTGAGCTTCCAAAGTGTGGATTAACAGGCGTAGAGCCACTCA 1195
Db	599 CAGGAGAACCGCCACACTTAGTACGCTCCCAAGTGTCTGGATTACAGGCGTAGAGCCACTCA 658
Db	539 TATTTTATAGCAAGATGGGGGTTTATACATGCTGGCCAGGCTGTCTTGAACCTCTACAT 598
Db	1076 TATTTTATAGCAAGCGGGGTTTACACATATTTGTAGAGCTGGTCTCAAACTCCTACCT 1135
Db	479 TCAGCGCTTCCAAATGAGTCTGGGATTCAGAGTGGCCACACAGCGCTGACTATTTTGG 538
Db	1018 TCAGCC-TCGCAAGCAGCTGGGATTAACGGGCACTGGCCACACACACCCCGCTA-ATTTTGG 1075
Db	419 AGTGAAGCATCTCGGCTCAGTCAACCTCCGCTGCTGGTTCAAGATTCCTCTGCC 478
Db	958 AATGGCAATCTCGGCTCAGTCAACCTCTGCTCCGAGGCTCAAGCAATCTCCTGTC 1017
Db	365 CACT-----TATTTTATTTTGTGAATGATGATCTACACTGCTACCTGCGGGAGTGC 418
Db	898 TTAATTTTATTTTGTGTGTTGTTGAATGGAATTCACCTCTGTTACCAGGGCGGGAGTGC 957
Db	305 ATCTGCTGCTCCGCGCTCCCAAAGTGTGGGATTCAGAGCTTGAGCCACCGCACCCGCG 364
Db	838 ATCTGCTGCTCCGCGCTCCCAAAGTGTGGGATTCAGAGCTTGAGCCACCGCACCCGCG 897
Db	245 TTTTATAGAGAGCGGGTTTACCGCTTATAGCAGATGCTGTGATCTCTGACCTGTG 304
Db	779 TTTTATAGAGAGGGG-TTCACCATGTTGCGCAGGTTGATGTTGATCTCTGACCTGTG 837
Db	185 CTTCCCGATACCTGTGATTAACAGGGGTTGCGCACACCGCCGACTAATTTTGTATTT 244
Db	722 CCTCTGATGACTGGGACTACAGGG---CCACACGCGCTAGCAATTTTGTATTT 778
Db	1196 CCCAGCCGCGTAA 1208
Db	659 CCTGGCCGCAAA 671
Db	1136 CAGGAGACCACCTGCTGAGCTTCCAAAGTGTGGATTAACAGGCGTAGAGCCACTCA 1195
Db	599 CAGGAGAACCGCCACACTTAGTACGCTCCCAAGTGTCTGGATTACAGGCGTAGAGCCACTCA 658
Db	539 TATTTTATAGCAAGATGGGGGTTTATACATGCTGGCCAGGCTGTCTTGAACCTCTACAT 598
Db	1076 TATTTTATAGCAAGCGGGGTTTACACATATTTGTAGAGCTGGTCTCAAACTCCTACCT 1135
Db	479 TCAGCGCTTCCAAATGAGTCTGGGATTCAGAGTGGCCACACAGCGCTGACTATTTTGG 538
Db	1018 TCAGCC-TCGCAAGCAGCTGGGATTAACGGGCACTGGCCACACACACCCCGCTA-ATTTTGG 1075
Db	419 AGTGAAGCATCTCGGCTCAGTCAACCTCCGCTGCTGGTTCAAGATTCCTCTGCC 478
Db	958 AATGGCAATCTCGGCTCAGTCAACCTCTGCTCCGAGGCTCAAGCAATCTCCTGTC 1017
Db	365 CACT-----TATTTTATTTTGTGAATGATGATCTACACTGCTACCTGCGGGAGTGC 418
Db	898 TTAATTTTATTTTGTGTGTTGTTGAATGGAATTCACCTCTGTTACCAGGGCGGGAGTGC 957
Db	305 ATCTGCTGCTCCGCGCTCCCAAAGTGTGGGATTCAGAGCTTGAGCCACCGCACCCGCG 364
Db	838 ATCTGCTGCTCCGCGCTCCCAAAGTGTGGGATTCAGAGCTTGAGCCACCGCACCCGCG 897
Db	245 TTTTATAGAGAGCGGGTTTACCGCTTATAGCAGATGCTGTGATCTCTGACCTGTG 304
Db	779 TTTTATAGAGAGGGG-TTCACCATGTTGCGCAGGTTGATGTTGATCTCTGACCTGTG 837
Db	185 CTTCCCGATACCTGTGATTAACAGGGGTTGCGCACACCGCCGACTAATTTTGTATTT 244
Db	722 CCTCTGATGACTGGGACTACAGGG---CCACACGCGCTAGCAATTTTGTATTT 778
Db	1196 CCCAGCCGCGTAA 1208
Db	659 CCTGGCCGCAAA 671
Db	1136 CAGGAGACCACCTGCTGAGCTTCCAAAGTGTGGATTAACAGGCGTAGAGCCACTCA 1195
Db	599 CAGGAGAACCGCCACACTTAGTACGCTCCCAAGTGTCTGGATTACAGGCGTAGAGCCACTCA 658
Db	539 TATTTTATAGCAAGATGGGGGTTTATACATGCTGGCCAGGCTGTCTTGAACCTCTACAT 598
Db	1076 TATTTTATAGCAAGCGGGGTTTACACATATTTGTAGAGCTGGTCTCAAACTCCTACCT 1135
Db	479 TCAGCGCTTCCAAATGAGTCTGGGATTCAGAGTGGCCACACAGCGCTGACTATTTTGG 538
Db	1018 TCAGCC-TCGCAAGCAGCTGGGATTAACGGGCACTGGCCACACACACCCCGCTA-ATTTTGG 1075
Db	419 AGTGAAGCATCTCGGCTCAGTCAACCTCCGCTGCTGGTTCAAGATTCCTCTGCC 478
Db	958 AATGGCAATCTCGGCTCAGTCAACCTCTGCTCCGAGGCTCAAGCAATCTCCTGTC 1017
Db	365 CACT-----TATTTTATTTTGTGAATGATGATCTACACTGCTACCTGCGGGAGTGC 418
Db	898 TTAATTTTATTTTGTGTGTTGTTGAATGGAATTCACCTCTGTTACCAGGGCGGGAGTGC 957
Db	305 ATCTGCTGCTCCGCGCTCCCAAAGTGTGGGATTCAGAGCTTGAGCCACCGCACCCGCG 364
Db	838 ATCTGCTGCTCCGCGCTCCCAAAGTGTGGGATTCAGAGCTTGAGCCACCGCACCCGCG 897
Db	245 TTTTATAGAGAGCGGGTTTACCGCTTATAGCAGATGCTGTGATCTCTGACCTGTG 304
Db	779 TTTTATAGAGAGGGG-TTCACCATGTTGCGCAGGTTGATGTTGATCTCTGACCTGTG 837
Db	185 CTTCCCGATACCTGTGATTAACAGGGGTTGCGCACACCGCCGACTAATTTTGTATTT 244
Db	722 CCTCTGATGACTGGGACTACAGGG---CCACACGCGCTAGCAATTTTGTATTT 778
Db	



